Description

B

Match Length

Score

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	
version - 2004	model
GenCore version 5.1.6 (c) 1993 - 2004 Compug	ws buisn
Copyright	OM nucleic - nucleic search, using sw model
	OM nucleic -

(without alignments) 6623.438 Million cell updates/sec 638 1 gaattegggaaegegecaca......ectgaatttgtaageaaett 638 August 24, 2004, 17:45:39 ; Search time 4175 Seconds IDENTITY_NUC Gapop 10.0 , Gapext 1.0 US-10-022-554A-3 Title: Perfect score: Scoring table: Sequence: Run on:

6940544 3470272 seqs, 21671516995 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database

gb_sts:* gb_sy:* gb_un:* gb_vi:* em_ba:* em_fun:* em hum:* em_pat:* gb ba:*
gb_htg:*
gb_om:*
gb_ow:*
gb_bv:*
gb_ph:*
gb_pl:*
gb_pr:* em_in:* em_mu:* em_om:* em_or:* em_ph:* em_pl:*

em sts:*
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em tig.hum:*
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em htg.g.nus:* em htgo other:* htgo_hum: * em htgo mus:* em_sy:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query

Result

A99428 Sequence 1 108499 Sequence 13 109297 Sequence 10 AR428605 Sequence AX481449 Sequence AX0328 Artificial A00329 Artificial S67291 Homo sapien BC037601 Mus muscu U67610 Mus musculu X4222 Rat mRNA fo X60317 S.scrofa ac A00069 Artificial A00070 Artificial B02757 DNA encodin B03743 CDNA encodin B03443 Synthetic c B03692 CDNA encodi E04557 Human aFGF E38006 Process for E38006 Process for E38006 Process for IO8090 Sequence 4 IO9138 Sequence 3 X13221 Bovine mRNA AR380845 Sequence Process for Sugar chain Process for Process for Sugar chain Sugar chain Bovine acid Process for Sugar chain 102042 Sequence 5 108496 Sequence 7 M13361 Human beta-H.sapiens a BC032697 Homo sapi Human mRNA X65778 | M35608 | X14032 | E38006 E26527 E38005 E26526 E37983 E37984 E37985 E26522 E26523 E26509 E26524 X51943 A49428 108499 108297 AR428605 A4481449 A00122 A00122 A00129 ECCTF010 RMHG/F10 RMHG/F1 SARC/ENA A00069 A00069 A00070 ECCTFO ECCTF 108496 HUMECGFB BC032697 HSHPGF1 108090 I09138 BTFGFAR AR380845 HSAFGF BOVFGFAA BTEDGF E26527 E38005 E26526 E37983 E26510 E26523 E26509 E26524 638 638 1073 2259 2259 638 490 490 490 668 668 72.1 72.1 72.1 68.1 67.7 66.2 7.49 549.8 549.8 4491.8 485.2 474.2 474.2 463.2 412.8 412.8 412.8 412.8 412.8 412.8 412.8 400.2 397.8 397.6 397.4 397.2 397.2 397.2 460 422.4

ALIGNMENTS

linear PAT 21-MAY-1993 3; Indels 0; Gaps 1 (bases 1 to 638)
Jaye,M., Burgess,W., Maciag,T. and Drohan,W.
Recombinant DNA vector encoding human endothelial cell growth Query Match 99.2%; Score 633.2; DB 6; Length 638; Best Local Similarity 99.5%; Pred. No. 7.9e-169; Matches 635; Conservative 0; Mismatches 3; Indels 0; Rorer Biotechnology, Inc.; King of Prussia, Location/Qualifiers 102042 638 bp ss-DNA Sequence 5 from Patent US 4868113. /organism="unknown" /wol_type="unassigned DNA" Patent: US 4868113-A 5 19-SEP-1989; 102042 102042.1 GI:270417 1. .638 Unclassified. Unknown. Unknown. factor DEFINITION ACCESSION VERSION source ORGANISM AUTHORS TITLE RESULT 1 102042 LOCUS REFERENCE JOURNAL KEYWORDS FEATURES ORIGIN

18.1 GGACAAGGGACCACCAGCACATTCAGCTGCAGCTGGGGAAAGCGTGGGGGGGG	Db 361 ATTACAACACCTATATATCCAAGAAGCATGCAGAAGAATTGGTTTGTTGGCCTCAAGA 420 Qy 421 AGAATGGGAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAACCAATCTTGTTTG Db 421 AGAATGGGAGCTGCAAACGCGGTCCTCGGACTCATGGCCAGAAACAATCTTGTTTC 480 Qy 481 TCCCCTGCAGTCTTTTCTGATTAAAGAATTCTTCTGGTGTTGACCACTCAGAGAA 540 Db 481 TCCCCTGCAGTCTTTTTTAAAGAATTCTTCTGGTGTTGACCACTCAGAGAA 540 Qy 61 GTTTTCGAGGGTCCTCACTTGATTAAAGAATTCTTCTGGTGTTGACCATTGGTGTGT 600 Qy 61 GTTTTCGAGGGTCCTCACTTGATTAAAGAATTGTTCCCTTTGACCATTGGTGGTG 600 Qy 61 GTTTTCGAGGGTCCTCACTTGATTAAAAATGTTCCCTTTGACCATTGGTGGCT 600 Qy 61 GTTTTCGAGGGTCCTCACTTGATTAAAAATTGTTCCCTTTGACCATTGGTGGCT 600 Qy 61 GTTTTCGAGGGTCCTCACTTGATTAAAAATTTTCCTTTGACCATTGGCTGGC	09	ORGANISM Homo sapiens Bukaryota: Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota: Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE 1 (bases 1 to 638) AUTHORS Jaye, M., How, R. R. Burgess, M., Ricca, G.A., Chiu, I.M., Ravera, M.W., O'Brien, S.J., Modi, W.S., Maciag, T. and Drohan, W.N. TITLE Human endothelial cell growth factor: cloning, nucleotide sequence, and chromosome localization JOURNAL Science 233 (4763), 541-545 (1986) MEDLINE 86261805 PUBMED 353756 COMMENT COMM	cribed from the same gene.	/tissue_trip="brain stem" /tissue_trip="brain stem" 39506 /codon_start=1 /product="beta-endothelial cell growth factor" /procedin_id="AAA79245.1" /db_xref="Gr:sla1942" /transla10:="WABGETITFTALIEKENIAPGGNYKKPKILYCSNGGHFIRILPDG	y Match
	Qy 241 AGGTGTATATAAAGAGTACCGAGACTGGCCAGGACACGGACACGGACACGACGCTTT 300 Db 241 AGGTGTATATAAAGAGTACCGAGACTGGCCATGGCCATGGACACCCGAGGGCTTT 300 Qy 301 TATACGACACACACAAATGGCGAATGTTTGTTCCTGGAAAGGCTGGAGAACC 360 Db 301 TATACAACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGAACC 360 Qy 361 ATTACAACACCTATATATCCAAGAAGCAGAAGAATTGTTGTTGTGCCTCAAGA 420 Db 361 ATTACAACACCTATATATCCAAGAAGCAGAGAAATTGTTTGT	Qy 481 TCCCCCTGCCAGTCTTCTGATTAAAGAATCTGTTCTGGTGTTGACCACTCCAGAGAA 540 Db 481 TCCCCCTGCCAGTCTTCTGATTAAAGAGATCTGTTCTGT	RESULT 2 108496 638 bp DNA linear PAT 02-DEC-1994	rce 1638 /organism="unknown" /mol_type="unassigned DNA" Match 99.2%; Score 633.2; DB 6 ocal Similarity 99.5%; Pred. 00.7.9e-169	GATTCGCGAACGCCCCACAACGCGCTCCTGAGCCATGGCTGAAGGGGAAATCACCA 60 GAATTCGCGAACGCCCCACAACGCGCTCGCTGAGCCATGGCTGAAGGGGAAATCACCA 60 GAATTCGCGAACGCCCCACAACGCAGCTGCTGAGCCTTGGCTGAAGGGGGAAATCACCA 60 GAATTCGCGAACGCCCTCAACGCAGCTGCTTGGCTCCAGGGGAATTACAAGAAGCCCAAG 12	DD 121 TCCTCTACTACTACTACTACTCTCTTACTACTTCTTCCGATGCACACTGCATGCA

Strausberg, K.L., Reingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Magner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, M.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleron, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Milahy, S.J., Bosak, S.A., McMan, P.J.,
McKernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wizny, D.M., Sodergren, E.J., Luk, Y. Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Roung, A.C., Shevchenko, Y.,
Boutfactic, G., Rabiseley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Kraywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. PRI 06-0CT-2003 1073 bp mRNA linear PRI 06-OCT-200:
Homo sapiens fibroblast growth factor 1 (acidic), mRNA (cDNA clone MGC:44867 IMAGE:5403677), complete cds.
BC032697 481 TCCCCCTGCCAGTCTCTTCTGATTAAAGAGATCTGTTCTGGTGTTGACCACTCCAGAGAA 540 241 AGGIGIATATAAAAGAGIACCGAGACIGGCCAGIACIIIGGCCAIGGACACCGACGGGCIIII 300 301 TATACGGCTCACACACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACC 360 361 ATTACAACACCTATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGCCTCAAGA 420 361 ATTACAACACCTATATATCCAAGAAGCATGCAGAAGAATTGGTTTGTTGGCCTCAAGA 420 421 AGAATGGGAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTC 480 481 TCCCCCTGCCAGTCTCTGATTAAAGAGATCTGTTCTGGTGTTGACCACTCCAGAGAA 540 541 GITICGAGGGICCICACCIGGITGACCCCAAAAIGIICCCIIGACCAIIGGCIGCGCI 600 541 GITICGAGGGTCCTCACCTGGTTGACCCCAAAATGTTCCCTTGACCATTGGCTGCGCT 600 61 CCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAC 120 61 CCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAC 120 121 TCCTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGCCACAGTGGATG 180 181 GGACAAGGGACAGGAGCGACCAGTACAGCTGCAGCTCAGTGCGGAAAGCGTGGGGG 240 241 AGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTT 300 301 TATACGGCTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACC 360 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 1073) 121 TCCTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATG 180 9 1 GAATTCGGGAAACGCGCCACAAGCAGCAGCTGCTGAGGCCATGGCTGAAGGGGAAATCACCA 60 1 GAATTCGGGAACGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCA 601 AACCCCCAGCCCACAGAGCCTGAATTTGTAAGCAACTT 638 601 AACCCCCAGCCCACAGAGCCTGAATTTGTAAGCAACTT 638 BC032697.1 GI:21595686 Homo sapiens (human) DEFINITION ORGANISM ACCESSION VERSION KEYWORDS REFERENCE AUTHORS BC032697 SOURCE 셤 셤 à 셤 ò ద à g ð 윰 à g ò 유 ò ద à ð ö ò

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/tränslation="maegeITTFTALTEKFNLPPGNYKKPKLLYCSNGGHFLRILPDG
TVDGTRDRSDQHIQLQLSAESVGEVYIKSTETGQYLAMDTDGLLYGSQTPNEECLFLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth factors are a family of proteins involved in growth and differentiation in a wide range of contexts. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: nisc_mgc@nhgri.nih.gov
Mklter,N. Ayele,K., Beckstrom-Sternberg,S.W., Benjamin,B.,
Blakesley,R.W. ayelle,K., Beckstrom-Sternberg,S.W., Brinkley,C., Brooks,S.,
Dietrich,N.L., Grante,S., Guan,X., Gupta,J., Haghighi,P.,
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Maduro,Q.L., Masiello,C., Maskerl,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth factors cause dimerisation of their tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     passed the following selection criteria: matched mRNA gi: 15055546.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="FGF; Region: Fibroblast growth factor. Fibroblast
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                                                                                                                                                                                                                                                                Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov
Series: IRAK Plate: 69 Row: d Column: 4
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECGF, ECGFA, ECGFB, HBGF1,
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Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine kinase receptors for
                                                                   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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ECGF-beta, FGF-alpha, GLIO703"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Young, A., Zhang, L.-H. and Green, E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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                                   human and mouse cDNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab host="DH10B'
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                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                       JOURNAL
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Indels

7.9e-169;

99.5%;

635; Conservative

Matches

Best Local Similarity

Pred. No. 7.96 0; Mismatches 2

Gaps

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Indels

6;

0; Mismatches

Best Local Similarity 98.7 Matches 627; Conservative

Query Match

94.3%; Score 601.4; DB 9; Length 1073; 98.7%; Pred. No. 9e-160;

	SULT 6 8090 CUS CUS CUS TOSITION RESTON YMORDS ORGANISM	factor. Homo sapiens (human) Memo sapiens (human) Homo sapiens (human) Memo sapiens (human) Homo sapiens (human) S. Homo sapiens (human) Eukarsapican Heraza, Craniata, Vertebrata, Butel Bukaryota, Metazaa, Chordata, Craniata, Vertebrata, Butel Mammalia, Eutheria, Primates; Catarthini, Hominidae, Homo E 1 (bases 1 to 2259) Miternative splicing generates two forms of mRNA coding for heparin-binding growth factor 1 L Oncogene 5 (5), 755-762 (1990) E 9025518 D 1693186 C Chiu, I.M. C Chiu, I.M. Dept of Internal Medi L Submitted (20-FBB-1990) Chiu IM., Dept of Internal Medi L Submitted (20-FB-1990) Chiu IM., Dept of Internal LM., Dept of In
		HSHPGFL 1 HSHPGFL 2259 bp mRNA linear TION Human mRNA for human heparin-binding growth factor. 10N X51943 S X51943 S X51943 S X51943 S Kibroblast growth factor; growth factor; heparin-bin Factor. Homo sapiens (human) NISM Homo sapiens (human) Elekaryota, Metazoa, Chordata, Craniata; Vertebrata; Elekaryota, Metazoa, Chordata; Craniata; Vertebrata; Elekaryota, Metazoa, Chordata; Craniata; Homoinidae.
181 AAC 245 GTZ 241 GTZ 305 CGC	D C C C C C C C C C C C C C C C C C C C	0y 544 TCGAGGGGTCCTCACCTGGTTGACCCTAAAATGTTCCCTTGACCATTGGCTGCGCTAAC 603
61 CAC 125 CTP 121 CTP 185 AAC		TGGGAGCTGGAAAGGGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTGT
627; 5 TCG 1 TCT 65 CAC	Matches	CGGCTCACAGACCAAATGACGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCATTA [
ch 1 Simi	ORIGIN Query Match Best Local Simi	OY 245 GTATATAAAGAGTACCGAGAACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATA 304
eature	misc_feature polyA_site	OY 185 AAGGACAGAGCACCAGCACACTTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGGGT 244
eature	misc_feature	Oy 65 CACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGAATTACAAGAAGCCCAAACTCCT 124 Db 117 CACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGAATTACAAGAAGCCCAAACTCCT 176 Qy 125 CTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGGAC 184 Db 177 CTACTGTAGCAACGGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGGAC 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear PAT 02-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACACCTATATATCCAAGAAGCATGCAGAGAATTGGTTTGTTGGCCTCAAGAAA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39GAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTCTCCC 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388AGCTGCAAACGCGGTCCTCGGACTCACTATGGCCAGAAAGCAATCTTGTTTCTCCC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGCCAGICTCTTCTGAITAAAGAGAICTGTTCT-GGIGITGACCACTCCAGAGAAGIT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCCAGTCTCTTCTGATTAAAGAGATCTGTTCTGGGTGTTGACCACTCCAGAGAAGTT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGAGGGCTCCTCACCTGGTTGACCCCAAAAATGTTCCCTTGACCATTGGCTGCGCTAAA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGAATTACAAGAAGCCCAAACTCCT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGGAC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGACAGGAGGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGAGGT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGACAGGAGCGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGAGGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGGCGGCTTTTATA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCATTA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGAACGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITGAAAGCGCCACAAGCAGCAGCTGAGCCATGAGGGAAAAGGGGAAAATCACCATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                               94.3%; Score 601.4; DB 9; Length 2259;
illarity 98.7%; Pred. No. 9.2e-160;
Conservative 0; Mismatches 6; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGCCCACAGAGCCTGAATTTGTAAGCAACTT 638
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(bases 1 to 638)
des,J.C., Abraham,J.A. and Protter,A.
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                                                                                                                                                                                                       /note="ex1/ex2 splice site" 307. .308
                                                                                                                                                                                                                                                        /note="ex2/ex3 splice site"
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uence 4 from Patent EP 0298723.
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                                                                                                                                                                                                                                                                                                             /note="polyA site"
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3090.1 GI:589198
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35. .502 /note="unnamed protein product; HBGF-1 (AA 1-155)"

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918. .1385 CDS 2; PAT 02-DEC-1994 55 AGTCTTGAAAGCGCCACAAGCAGCAGCTGCTGAGGCCATGGCTGAAGGGGGAAATCACCACC 114 355 TACGGCTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAAACAT 414 475 AATGGGAGCTGCAAACGCGGTCCTCGGACTCACTATGGCCAGAAAGCAATCTTGTTTCTC 534 55 AGTCTTGAAAGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACC 114 63 ITCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTC 122 115 TTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTC 174 123 CTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGG 182 183 ACAAGGGACAGGAGCGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGAG 242 235 ACAAGGGACGGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTAGGGGGAG 294 243 GIGIATATAAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTA 302 295 GTGTATATAAAGAGTACCGAGACTGGCCAGTAGCTTGGCCATGGACACCGAGGGCTTTTA 354 303 TACGGCTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCAT 362 363 TACAACACCTATATATCCAAGAAGCATGCAGAAGAATTGGTTTGTTGGCCTCAAGAAG 422 423 AATGGGAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTCTC 482 483 CCCCTGCCAGTCTCTTCTGATTAAAGAGATCTGTTCT-GGTGTTGACCACTCCAGAGAAG 541 3 ATTOGGGAACGCGCCACAAGCAGCAGCTGCTGAGCCATGACTGAAGGGGAAATCACCACC 62 3 ATTCGGGAAACGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACC 62 Query Match 86.2%; Score 549.8; DB 6; Length 638; Best Local Similarity 98.5%; Pred. No. 4.2e-145; Matches 576; Conservative 0; Mismatches 7; Indels 2; Gaps Gaps 2; Query Match 86.2%; Score 549.8; DB 6; Length 638; Best Local Similarity 98.5%; Pred. No. 4.2e-145; Matches 576; Conservative 0; Mismatches 7; Indels 2; 542 TITICGAGGGGTCCTCACCTGGTTGACCCCCAAAATGTTCCCTTGA 586 linear Unclassified.

1 (bases 1 to 638)
Fiddes,J.C., Abraham,J.A. and Protter,A.
Patent: WO 8900198-A 3 12-JAN-1989;
Location/Qualifiers DNA Recombinant fibroblast growth factors Patent: EP 0298723-A1 4 11-JAN-1989; Location/Qualifiers /organism="unknown" /mol_type="unassigned DNA" /organism="unknown" /mol_type="unassigned DNA" 109138 638 bp Sequence 3 from Patent WO 8900198. I09138.1 GI:588154 1. .638 1. .638 Unknown. Unknown source TITLE JOURNAL FEATURES DEFINITION ORGANISM AUTHORS JOURNAL FEATURES ACCESSION VERSION RESULT 7 I09138 KEYWORDS REFERENCE ORIGIN ORIGIN ò g ò g à g ò g à g ö à g à à g g ò g ò q

55 Dp	TICACAGCCCTGACCGAGGAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTC 17
δ _γ 1	123 CTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGG 182 [17] [
Qy 1	183 ACAAGGGACAGGACCAGCACAGACAGACTTCAGCTGCAGTCAGT
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Qy 4	423 ANTGGGAGCTGCAACGCGGTCCTRAAACTCACTATGGCCAGAAACCTTGTTTCTC 482
yo da	483 CCCCTGCCAGTCTCTTCTGATTAAAGAGTCTGTTCT-GGTGTTGACCACTCCAGAGAAG 541
	TITICGAGGGGTCCTCACCTGGTTGACCCCAAAATGTTCCCTTGA 586
BEFGEAR LOCUS DEFINITION ACCESSION VERSION VERYWORDS SOURCE ORGANISM	nena linear Mam 18-NOV-19: rowth factor. owth factor. sata; Vertebrata; Euteleostomi;
REFERENCE AUTHORS TITLE JOURNAL MEDLINE	Pecora; rowth fa
PUBMED REFERENCE AUTHORS TITLE	3205724 2 Philippe, J.M., Renaud, F., Desset, S., Laurent, M., Mallet, J., Courtois, Y. and Edwards, J.B. Cloning of two different 5' untranslated exons of bovine acidic fibroblast growth factor by the single strand liquion to
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	1280126 3 (bases 1 to 4005) Halley,C.
	Direct Submission Submitted (12-OCT-1988) Halley C., Inserm UI18, 29 Rue Wilhem 75016, Paris, France
COMMENT FEATURES	0.
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93

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1008 TGCAGCAACGGGGGCTACTTCCTGAGAATCCTCCCAGATGGCACAGTGGGATGGGACGAAG 1067 1068 GACAGGAGCGACCACCATTCAGCTGCAGCTCTGTGCGGAAAGCATAGGGGAGGTGTAT 1127 1188 TCACAGACACCCAATGAGGAATGTTTGTTCCTGGAAAGGTTGGAGGAAAACCATTACAAC 1247 1308 AGGTCTAAACTCGGTCCTCGGACTCACTTCGGCCAGAAAGCCATCTTGTTTCTCCCCCTG 1367 488 308 189 GACAGGAGGGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAAGCGTGGGGGAGGTGTAT 248 309 TCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCATTACAAC 368 369 ACCTATATATCCAAGAAGCATGCAGAAGAATTGGTTTGTTGGCCTCAAGAAGAATGGG 428 69 GCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTAC 128 129 TGTAGCAACGGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGGACAAGG 188 9 GAACGCGCCACAAGCAGCAGCTGCTGAGCCATGCTTGAAGGGGAAATCACCACCTTCACA 68 249 ATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGC 429 AGCTGCAAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTCTCCCCCTG Gaps 2; Score 491.8; DB 4; Length 4005; Pred. No. 1.4e-128; 72; Indels 0; Mismatches 77.1%; 88.3%; 557; Conservative Similarity Query Match Best Local Matches

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1428 GGGGTCCTCACCTGGCTGACCCC-AGAITGTACCCTTTACCATTGGCCGTGCTAACCCCT 1486 1368 CCAGTCTCCTCTGATTAAAGAAATCTGTTGTGGGGTGCTGACCACTCCAGAGGAATCTGAA 1427 548 GGGGTCCTCACCTGGTTGACCCCAAAAATGTTCCCTTGACCATTGGCTGCCTGAACCCCC 607 489 CCAGTCTCTTCTGATTAAAGAGATCTGTTCT-GGTGTTGACCACTCCAGAGAAGTTTCGA 1487 GGCCCACAGGGCCTAAACCTGTAAACGCGCTT 1517 608 AGCCCACAGAGCCTGAATTTGTAAGCAACTT 638 임 δ g à à

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RESULT 9 g

Sequence 1390 from patent US 6607879. AR380845 AR380845.1 GI:40088479 Unknown. DEFINITION ACCESSION AR380845 KEYWORDS VERSION SOURCE

PAT 18-DEC-2003

linear

DNA

1 (bases 1 to 490)
Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
Compositions for the detection of blood cell and immunological response gene expression Patent: US 6607879-A 1390 19-AUG-2003; Unclassified. ORGANISM REFERENCE AUTHORS TITLE

Location/Qualifiers /organism="unknown" .490 source

JOURNAL

FEATURES

ORIGIN

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ORIGIN

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Yu,Y.L., Kha,H., Golden,J.A., Migchielsen,A.A., Goetzl,E.J. and 181 TCACCTGCAGCTCAGTGCGGAAAGCGTGGGGGGGGTGTATAAAAGAGTACCGAGACTGG 29 CTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAA 1 CTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAA 89 TCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTT 149 CCTGAGGATCCTTCCGGATGGCACAGTGGACAGGGACAGGGACAGGACCAGCACAT 209 TCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGGGTGTATATAAAGAGTACCGAGACTGG 449 AACTCACTATGGCCAGAAAGCAATCTTGTTTCTCCCCCTGCCAGTCTCTTGATTAAAG Gaps fibroblast growth factor; fibroblast growth factor acidic. Homo sapiens (human) H.sapiens aFGF mRNA for acidic fibroblast growth factor. X65778 ; Length 490; /product="acidic fibroblast growth factor"
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/db.xref="SWISS-PROT:P05230" linear 3; Indels DB 6; Score 485.2; DB 6; Pred. No. 9.7e-127; mRNA 0; Mismatches /organism="Homo sapiens" 490 pb /db_xref="taxon:9606" Location/Qualifiers /mol_type="mRNA" /codon_start=1 76.1%; X65778.1 GI:396163 487; Conservative 509 AGATCTGTTC 518 1. .490 481 AGATCTGTTC 490 Homo sapiens Best Local Similarity 1372643 HSAFGF Query Match DEFINITION ACCESSION VERSION source ORGANISM RESULT 10 HSAFGF Matches REFERENCE AUTHORS JOURNAL MEDLINE PUBMED 9 KEYWORDS FEATURES TITLE SOURCE 임 à g 셤 ð 쉽 ò 셤 ò 임 à a à ò d à 셤 à

Query Matches 44 Matches 44 Db	n 76.1%; Score 485.2; DB 9; Length 490; Similarity 99.4%; Fred. No. 9.7e-127; Indels 0, Gaps 0; 37; Conservative 0; Mismatches 3; Indels 0, Gaps	9 CTCCTGAGCCATGGCTGAAGGGGAAATCACCACCTCACCAGCCCTGACCGAGAGTTTAA 88	9 TCTGCCTCCAGGGAATTACAAGAGCCAAACTCCTCTACTGTAGCAAGGGGGGGCCACTT 148	9 CCTGAGGATCCTTCCGGATGGCACAGTGGATGGGACAAGGACAGCACAGCACACAGT 208	9 TCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGGGCTGTATATAAAGAGTACCGAGACTGG 268	9 CCAGTACTTGGCCATGGACACCGGCGTTTTATACGGCTCACAGACACCAAATGAGGA 328	9 ATGITICTICCTGGAAGGCTGGAGGACCATTACAACACCTATATATCCAAGAAGCA 388	9 TGCAGAGAAATTGGTTTGTTGGTCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCTAA 448	9 AACTCACTATGGCCAGAAAGCAATCTTGTTTCTCCCCCTGCCAGTCTCTTCTGATTAAAG 508	9 AGAICHTIC 518 1 AGAICHTIC 490	BOVPGFAA Bovine acidic eye-derived fibroblast growth factor (EDGP II) mRNA, complete cds. M35608 - 1 Gill63047 M35608 - 1 Gill63047 M35608 - 1 Gill63047 Bos taurus (cow) Bos taurus (cow) Bos taurus Bukaryota, Matazoa; Chordata, Craniata; Vertebrata; Euteleostom; Mamalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bowidea; Bosinea; Bovinea; Bosinea; Bosine and its expression in brain and retina acidic PGF cDNA clone and its expression in brain and retina acidic PGF cDNA clone and its EDG Lett. 242 (1), 41-46 (1988) Bosinea; Bosinea; Bosinea; Bosine retina, cDNA to mRNA. Location/Qualifiers 1. 668 Location/Qualifiers 1. 668 Location/Qualifiers 1. 568 Location/Qualifiers 1. 568 Location/Qualifiers 1. 568 Location/Qualifiers 1. 668 Location/Qualifiers 1. 668 Location/Qualifiers 1. 668 Location/Qualifiers 1. 668 Location/Qualifiers 1. 7668 Location/Carsingea; Mamalia; Rocatived fibroblast growth factor" Codon start=1 Location/Carsingea; Mamalia; Location-Warderin; Abargeriters Mamalia; Location-Warderin; Abargeriters Mamalia; Location-Warderin; Mamalia; Mamalia; Location-Warderin; Mamalia; Mama	RLEENHYNTYISKKHAEKHWFVGLKKNGRSKLGPRTHFGQKAILFLPLPVSSD"
	atch cal	29 (899	149	209	269	329	389	449	509	Σ Σ U	!

ORIGIN

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BIEDGF 668 bp mRNA linear MAM 18-NOV-1993 Bovine mRNA for EDGF II (acidic eye-derived growth factor II).
                                                                                                                                                                             181 TGCAGCAACGGGGGCTACTTCCTGAGAATCCTCCCAGATGGCACAGTGGGAGGAAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                 481 AGGTCTABAACTCGGTCCTCGGACTCACTTCGGCCAGAAAGCCATCTTGTTTCTCCCCCTG 540
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                               301 ATTAAGAGTACGGAGACTGGCCAGTTCTTGGCCATGGACACCGACGGGCTTTTGTACGGC 360
                                                                                                                                                                                                                                                                                                                                                                                          309 TCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCATTACAAC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 ACCTATATATCCAAGAAGCATGCAGAAGAATTGGTTTGTTGCTCAAGAAGAATGGG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429 AGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTTCTCCCCCTG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 489 CCAGTCTTCTCTATTAAAGAGATCTGTTCTGG --TGTTGACCACTCCAGAGAAGTTTCG 546
                                 61 GAAACAGCCACAACCAGCAGCTGCTGAGGCCATGGCTGAAGGAGAAACCACGACCTTCACG 120
                                                                          69 GCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTAC 128
                                                                                                                                                        129 TGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGGACGAGG 188
                                                                                                                                                                                                                                                                                                              249 ATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGGACGGCTTTTATACGGC 308
9 GAACGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Philippe, J.M., Renaud, F., Desset, S., Laurent, M., Mallet, J., Courtois, Y. and Edwards, JB.

Cloning and Edwards, JB.

Cloning of woulfferent 5' untranslated exons of bovine acidic fibroblast growth factor by the single strand ligation to single-stranded cDNA methodology

Biochem. Biophys. Res. Commun. 188 (2), 843-850 (1992)

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Alterio,J., Halley,C., Brou,C., Soussi,T., Courtois,Y. and
Laurent,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Characterization of a bovine acidic FGF cDNA clone and its
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74.3%; Score 474.2; DB 4; Length 668; 88.3%; Pred. No. 1.3e-123; tive 0; Mismatches 68; Indels 3; Gaps

Query Match
Best Local Similarity 88.3*
Matches 538; Conservative

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linear PAT 02-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 CTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGAAG 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468 AATTGGTTTGTTGGCCTCAAGAAGAATGGGACTGCAAACGCGGTCCTCGGACTCACTAT 527
                                                                                                                                                                                                                                                                                                                                                                                                              108 ATGCCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCA 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              528 GGCCAGAAAGCAATCTTGTTTCTCCCCTGCCAGTCTCTTCTGATTAAAGAGTCCG 584
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1 (bases 1 to 8501)
Cameron, B. and Cruset, J.
EMETHON FOR THE PRODUCTION OF RECOMBINANT PROTEINS, PLASMIDS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 CCATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTC
                                                                                                                                                                                                                                                                                                                                                                                    39 ATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAGTTTAATCTGCCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 8501;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
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                                                                                                                                                                                                                                                                                                                           Pred. No. 1.5e-122;
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Fiddes, J.C. and Abraham, J.A.
RECOMBINANT FIRROBLAST GROWTH FACTORS
Patent: WO 8701728-A 13 26-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                   Other publication AU 3475495 960329
Other publication FR 2724665 960322
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/mol_type="unassigned DNA"
                                                                                                                                                                                                                       /mol_type="unassigned DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                       73.8%; Score 470.6;
                                                                            Patent: WO 9608572-A 1 21-MAR-1996;
                                                                                                                                                                                                      /organism="unidentified"
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                                                                                                                                                                                                                                                                                                       /translation="MARGETTTFTALTEKFYLPLCNYKKPKLLYCSNGGYFLRILDDG
TVDGTKDRSDQHIQLQLCAESIGEVYIKSTETGQPLAMDTDGLLYGSQTPNEECLFLE
RLESNHYNTYISKKHAEKHWFVGLKKNGRSKLGPRTHFGQKAILFLPLPVSSD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GCCCTGACTGAGAGTTTAACCTGCCTCTAGGCAATTACAAGAAGCCCAAGCTCCTCTAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TGCAGCAACGGGGGCTACTTCCTGAGAATCCTCCCAGATGGCACAGATGGGACGAAG 240
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                                                                                                                                             91. .558
/note="unnamed protein product; acidic eye-derived growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GAAACAGCCACAACCAGCAGCTGAGCCATGGCTGAAGGAGAAACCACGACCTTCACG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCCAAACTCCTTAC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 TGTAGCAACGGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGGACAAGG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 GAACGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACACCACCTTCACA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 GACAGGAGCGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGAGTGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           547 AGGGGTCCTCACCTGGTTGACCCCAAAATGTTCCCTTGACCATTGGCTGCGCTAACCC
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/db_xref="GOA:P03968"
/db_xref="SWISS-PROT:P03968"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                           /protein_id="CAA32192.1"
                                                                                                                            /clone lib="lambda gtll"
                                                                                                                                                                                        Eactor II (AA 1 - 155)"
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/mol_type="mRNA"
                                                               /db_xref="taxon:9913"
                                                                                                      'tissue_type="retina"
                                                                                       /clone="11.32.12"
                                                                                                                                                                                                              /codon start=1
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660 TGGCCCACA 668
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		Sequence 10 from Patent WO 8902471. 109297. 109297.1 GI:588003 Unknown. Unclassified. 1 (bases 1 to 481) 1 (bases 1 to 481)	13.7%; Score 464; DB 6; Length 481; Similarity 98.9%; Pred. No. 1e-120; Fraction of the conservative 0; Mismatches 5; Indels 0; Conservative 0; Mismatches 5; Indels 0; Confoction of the conservation of the confoction o		
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9 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		RESULT 15 109297 1000US DEPINITION ACCESSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	Query Match Best Local Matches 46 Qy 37	6 6 6 6	6 8 6 8 6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Acf04029 Thrombin	Aan70788 Complete	Aat37503 Human bet	Aav34350 Human end	Aax01723 Human end	Acf04028 Thrombin	Aat45985 Human end	Acc42968 Human Fib	Abx63225 Human cDN	Aan93088 Acidic fi	Aat12907 Novel exp	Aan71029 Sequence	Aan90994 Partially	Abv78179 Human DNA	Abz35755 Human pol	Abx09998 Human DNA	Aak98918 Human aci	Abl91720 Human pol	Aaq03871 Synthetic
В	ACF04029	AAN70788	AAT37503	AAV34350	AAX01723	ACF04028	AAT45985	ACC42968	ABX63225	AAN93088	AAT12907	AAN71029	AAN90994	ABV78179	ABZ35755	ABX09998	AAK98918	ABL91720	AAQ03871
DB	8	1	7	7	~	89	~	60	7	7	7	Н	Н	9	9	9	9	9	7
* Query Match Length DB	638	638	638	638	638	638	639	2357	4087	638	8501	481	481	468	468	468	468	468	496
& Query Match	100.0	99.2	99.2	99.2	99.2	99.2	97.5	94.3	94.3	86.2	73.8	72.7	72.7	72.6	72.6	72.6	72.6	72.6	72.1
Score	638	633.2	633.2	633.2	633.2	633.2	622.2	601.8	601.8	549.8	470.6	464	464	463.2	463.2	463.2	463.2	463.2	460
Result No.	п	73	m	4	ហ	9	7	80	đ	10	11	12	13	14	15	16	17	1.8	19

73	0	457.2	71.7	462	~	AAT45983	Aat45983	Human end	
7	21	432	67.7	1216	6	ADB59173	Adb59173	Toxicity-	
71	22	432	67.7	1216	6	ADB52615	Adb52615	Primary r	
7	23	412.8	64.7	454	4	AAQ02421	Aaq02421	cDNA enco	
7	4	412.8	64.7	454	7	AAQ03873	Aaq03873	Synthetic	
7	'n		64.7	454	~	AAQ10399	Aaq10399	Human aci	
7	9	412.8	64.7	454	N	AAQ10166	Aaq10166	Human aci	
7	7	412.8	64.7	454	N	AAQ25916	Aaq25916	afGF mute	
7	00	407	63.8	707	σ	ADD68686	Add68686	DNA ampli	
7	6	404	63.3	434	σ	ADD68674	Add68674	Human DNA	
m	0	404	63.3	546	σ	ADD68675	Add68675	DNA ampli	
3	31	404	63.3	546	9	ADD68676	Add68676	DNA ampli	
٣	ŭ	400.2	62.7	408	6	ADD68672	Add68672	Human DNA	
3	5	400.2	62.7	537	٣	AAC66129	Aac66129	Mutant PG	
M	4	397.8	62.4	630	7	AAX81396	Aax81396	Polynucle	
٣	5	397.6	62.3	537	٣	AAC66128	Aac66128	Mutant FG	
M	9	397.4	62.3	516	7	AAX81395	Aax81395	Polynucle	
e	17	397.2	62.3	408	m	AAC66107	Aac66107	Human FGF	
m	89	397.2	62.3	525	7	AAX81379	Aax81379	Polynucle	
m	39	397.2	62.3	525	е	AAC66108	Aac66108	Chimeric	
4	40	397.2	62.3	525	m	AAC66109	Aac66109	Chimeric	
4,	41	397.2	62.3	900	7	AAX81392	Aax81392	Polynucle	
4	42	397.2	62.3	600	7	AAX81391	Aax81391	Polynucle	
4	43	397.2	62.3	602	6	ADD68692	Add68692	DNA ampli	
4.	44	397.2	62.3	647	σ	ADD68691	Add68691	DNA ampli	
4	45	97.	62.3	663	7	AAX81378	Aax81378	Polynucle	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New thrombin degradation resistant fibroblast growth factor-1 (FGF-1) polypeptide, useful for treating a disease or disorder, e.g. cerebral ischemia or bone damage, or for enhancing the effectiveness of an FGF-1
                                                                                                                                                                                                                                            Thrombin resistant FGF-1; FGF-1; fibroblast growth factor-1; mycoardial ischaemia; peripheral vascular disease; cerebral ischaemia; epithelial injury; epidermal wound injury; nerve injury; mutant; bone damage; vasotropic; cardiant; cerebroprotective; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drohan WN;
                                                                                                                                                                                                                           Thrombin resistant FGF-1 mutant coding sequence.
                                                                                                                                                                                                                                                                                                                                                                   /product= "FGF-1 mutant"
                                                                                                                                                                                                                                                                                                                                                                              'partial
'note= "no start codon"
                                                                                                                                                                                                                                                                                      neuroprotective; osteopathic; gene; ds
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Claim 1; Fig 10; 83pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 ATTACAACACCTATATATCCAAGAAGCATGCAGAAGAATTGGTTTGTTGGCCTCAAGA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TCCTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACGTGGATG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CCTTCACAGCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAC 120
             The present invention provides the protein and coding sequences of human thiorblast growth factor-1 (FGG-1) and a mutant that is resistant to thrombin degradation. The thrombin degradation resistant FGF-1 protein can be used for treating a disease or disorder (e.g. myocardial ischaemia, peripheral vascular disease, cerebral ischaemia, epithelial injury, nerve injury, or bone damage), for enhancing the effectiveness of an FGF-1 response, or for stimulating an FGF-1 response in a mammal. The present sequence is the mutant FGF-1
                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                          100.0%; Score 638; DB 8; Length 638; 100.0%; Pred. No. 1.1e-187; tive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                           Sequence 638 BP; 175 A; 164 C; 166 G; 133 T; 0 U; 0 Other;
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121 AGAATGGGAGCTGCAAACGCGGTCCTCGGACTCACTATGGCCCAGAAAGCAATCTTGTTTC 480
                                 TCCCCCTGCCAGTCTCTTCTGATTAAAGAGATCTGTTCTGGTGTTGACCACTCCAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                               Human beta-endothelial cell growth factor.
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/*tag= b
/label= beta-ECGF
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/label= alpha-ECGF
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/label= acidic_FGF
102. .503
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                                                                                                                                                                                                                                                                                 AAT37503 standard; DNA; 638 BP.
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29-APR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             To screen the human brain stem cDNA library for clones contg. ECGF inserts, a specific oligonucleotide was designed. This oligonucleotide was based upon a maino terminus of ECGF (see AAP70480 and AAP70481). Fig 3c sets forth for comparison the AA sequence of cyanogen bromide-cleaved bovine alpha and beta ECGF (AAP70834). The two clones that were isolated, ECGF clones 1 and 29, were analysed in further detail. The nucleotide sequence of these clones and the AA sequence deduced from the nucleic acid sequence is shown in Fig 8 (see AAN70788 and AAP70482). (Updated on 25-MAR-2003 to correct PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human endothelial cell growth factor - produced by recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.2%; Score 633.2; DB 1; Length 638; 99.5%; Pred. No. 3.5e-186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 Jaye M, Burgess W, Maciag T, Drohan W;
                                                                                                 /product= "Acidic FGF"
102. .506
                                                                                                                                                 /product= "Alpha ECGF"
                                              /product= "Beta ECGF"
84. .101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 techniques, useful for wound healing.
                                                                                                                                                                                                                                                                                                                                 (RORE ) RORER BIOTECHNOLOGY INC.
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Bovine beta-endothelial cell growth factor (beta-ECGF; AAW03999) having a mol.wt. of 20 kD can be purified at least 16300 fold from bovine brain using heparin-Sepharose affinity chromatography. ECGF is useful for, among other purposes, diagnostic applications and has potential in the treatment of damaged blood vessels or other endothelial cell-lined structures. Human ECGF (AAT37503) or fragments may be obtained using oligonucleotides (AAT37504 and AAT37508 to AAT37509) whose design is based on the sequence of bovine alpha- and beta-ECGF. (Updated on 25-WAR-2003 to correct PP field.)
                                              541 GTTTCGAGGGSTCCTCACCTGGTTGACCCCAAAATGTTCCCTTGACCATTGGCTGCGCT 600
481 TCCCCCTGCCAGTCTTCTCATTAAAGAGATCTGTTCTGGTGTTGACCACTCCAGAGAA 540
                                                                                                                                                                                                                                                                                                                                Endothelial cell growth factor; ECGF; blood vessel; regeneration;
heparin-Sepharose affinity chromatography; probe; oligonucleotide; FGF;
fibroblast growth factor; ss.
                               541 GTTTCGAGGGGTCCTCACCTGGTTGACCCCAAAAATGTTCCCTTGACCATTGGCTGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated, purified, biologically active bovine beta endothelial cell growth factor - useful to regenerate or treat damaged blood vessels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;
                                                                                                         601 AACCCCCAGCCCACAGAGCCTGAATTTGTAAGCAACTT 638
                                                                                          601 AACCCCCAGCCCACAGAGCCTGAATTTGTAAGCAACTT 638
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   Length 638;
                                                                 3; Indels
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/note= "endothelial cell growth factor"
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Score 633.2; DB 2;
Pred. No. 3.5e-186;
                     99.5%; Prea. ac.
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39. .506
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87US-00134499.
       99.2%;
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18-DEC-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 AGAATGGGAGCTGCAAACGCGGTCCTCGGACTCACTATGGCCAGAAAGCAATCTTGTTTC 480
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W75418). The ECGF protein can be used in compositions for promoting wound healing. ECGF is also used to grow cells on a prosthetic device
                                                                                                                                                                                                                                                                                                                                                                                                                       61 CCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 GGACAAGGGACAGGACCACCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 ATTACAACACCTATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGCCTCAAGA
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                                                                                                                                                                                                                                                                                         1 GAATTCGGGAACGCGCCACAACCACCACAGCTGCTGAGCCATGAGGGGAAATCACCA
                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                            99.2%; Score 633.2; DB 2; Length 638;
                                                                                                                                                                                                                              3; Indels
                                                                                             Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601 AACCCCCAGCCCACAGAGCCTGAATTTGTAAGCAACTT 638
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                                                                                                                                                                                               Pred. No. 3.5e-186;
                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                  99.5%;
                                                                                                                                                                                                                              Matches 635; Conservative
                                                                                                                                                                                               Similarity
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                                                                                                                                                                   Query Match
                                                                                                                                                                                                  Best Local
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AAX01723 standard; cDNA; 638 BP.

RESULT 5
AAX01723
ID AAX
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This sequence represents the complete cDNA sequence encoding both human alpha— and beta—endothelial cell growth factors (EGGF, AANY313-W7514). The sequence was isolated from a human brain stem cell cDNA library using a probe designed based on fragments of the bovine ECGF (see AAN75416-

endothelial cell

Compositions for promoting wound healing - containing

Example, Fig 8; 23pp; English.

growth factor polypeptides.

(RHON) RHONE-POULENC RORER PHARM INC. Jaye M, Burgess W, Maciag T, Drohan WN;

WPI; 1998-594032/50. P-PSDB; AAW75415.

91US-00693079. 91US-00799859. 94US-00334884. 95US-00472964.

29-APR-1991; 27-NOV-1991; 03-NOV-1994; 07-JUN-1995;

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181 GGACAAGGGACAGGAGGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAAGCGTGGGGG 240
                                                                                                                            TATACGGCTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACC 360
                                                                                                                                             TATACGCCTCACAGACACAAAATGAAGTTTTGTTCCTGGAAAGGCTGGAGAGAAACC 360
                                                                                                                                                                                                                       421 AGAATGGGAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTC 480
                                                                                                                                                                                                                                                                                                                     TCCCCCTGCCAGTCTCTTCTGATTAAAGAGATCTGTTCTGGTGTTGACCACTCCAGAGAA 540
                                                                                                                                                                                                                                                                                                                                                  TCCCCCTGCCAGTCTCTTCTGATTAAAGAGATCTGTTCTGGTGTTGACCACTCCAGGAA 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New thrombin degradation resistant fibroblast growth factor-1 (FGF-1) polypeptide, useful for treating a disease or disorder, e.g. cerebral ischemia or bone damage, or for enhancing the effectiveness of an FGF-1 response in a mammal.
                                                               241 AGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTT
                                                                              241 AGGTGTATATAAAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCCGACGGGCTTT
                                                                                                                                                                                                                                                                                      AGAATGGGAGCTGCAAACGCGGTCCTCGGACTCACTATGGCCCAGAAAGCAATCTTGTTTC
                                                                                                                                                                                                                                                                                                                                                                                  GTTTCGAGGGGTCCTCACCTGGTTGACCCCAAAAATGTTCCCTTGACCATTGGCTGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombin resistant FGF-1; FGF-1; fibroblast growth factor-1; myocardial ischaemia, pertipheral vascular disease; cerebral ischaemia, epithelial injury; epidermal wound injury; nerve injury; bone damage; vasotropic, cardiant; cerebroprotective; vulnerary; neuroprotective;
 GGACAAGGGACAGGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGG
                                                                                                                                                                                          ATTACAACACCTATATACCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGCCTCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombin resistant FGF-1 mutant production wildtype coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                601 AACCCCCAGCCCACAGAGCCTGAATTTGTAAGCAACTT 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "no start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MAIN-) MAINE MEDICAL CENT RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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/product= "FGF-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACF04028 standard; DNA; 638 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteopathic; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REPA-) REPAIR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W02003052378-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factors (ECGF) and plasmids comprising the DNA sequences. The DNA encodes a cleavable signal peptide and an ECGF, where removal of the signal peptide yields a mature form of the ECGF, where the ECGF is alpha-ECGF or beta-ECGF. The DNA is used to produce recombinant ECGF proteins, which can be used in treatments to repair or regenerate blood vessels or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTTCACAGCCCTGACCGAGAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTCTACTGTAGCAACGGGGGCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding a cleavable signal peptide and an endothelial cell growth factor - useful for producing recombinant endothelial cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              structures lined with endothelial cells. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human ECGF cDNA sequence (determined from lambda ECGF clones 1 and 29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAATTCGGGAAACGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCA
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                                                                                            Endothelial cell growth factor; ECGF; cleavable; recombinant; repair; regenerate; blood vessel; endothelial cell; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to DNA encoding human endothelial cell growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.2%; Score 633.2; DB 2; Length 638; 99.5%; Pred. No. 3.5e-186;
                                                                                                                                                                                                                                                                                                                                                  /*tag= d
/note= "alpha-ECGF begins at this position"
                                                                                                                                                                                                                                                                                                       /*tag= c
/note= "acidic FGF begins at this position"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                       /*tag= b
/note= "beta-ECGF begins at this position"
                                                               Human endothelial cell growth factor (ECGF) cDNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jaye M, Burgess W, Maciag T, Drohan WN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RHON ) RHONE-POULENC RORER PHARM INC.
                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 8; 23pp; English
                                                                                                                                                                                                                        /product= "ECGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87US-00134499.
91US-00693079.
91US-00799859.
94US-00334884.
95US-00472964.
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                                20-APR-1999 (first entry)
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                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      900
                                The present invention provides the protein and coding sequences of human that ast growth factor-1 (RGF-1) and a mutant that is resistant to thrombin degradation. The thrombin degradation resistant FGF-1 protein can be used for treating a disease or disorder (e.g. myocardial ischaemia, peripheral vascular disease, cerebral ischaemia, epithelial injury, nerve injury, or bone damage), for enhancing the effectiveness of an RGF-1 response, or for stimulating an RGF-1 response in a mammal. The present sequence is the wildtype FGF-1
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                                                                                                                                                                                                                                                                                                                                                                            GAATTCGGGAACGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 AGAATGGGAGCTGCAAACGCGGTCCTCGGACTCACTATGGCCAGAAAGCAATCTTGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCCCCTGCCAGTCTCTTCTGATTAAAGAGATCTGTTCTGGTGTTGACCACTCCAGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 GTTTCGAGGGGTCCTCACCTGGTTGACCCCCAAAAATGTTCCCTTGACCATTGGCTGCGCT
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                                                                                                                                                                                                                                                               Score 633.2; DB 8; Length 638; Pred. No. 3.5e-186; 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                            Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 AACCCCCAGCCCACAGAGCTGAATTTGTAAGCAACTT 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              601 AACCCCCAGCCCACACAGAGCCTGAATTTGTAAGCAACTT 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human endothelial cell growth factor cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endothelial cell growth factor; ECGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
Claim 2; Fig 8; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT45985 standard; cDNA; 639
                                                                                                                                                                                                                                                                 99.2%;
                                                                                                                                                                                                                                                                                   99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                     Matches 635; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003 (revised)
                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                          coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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Jaye M, Maciag T, Burgess

Drohan WN,

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WPI; 1996-505421/50.

P-PSDB; AAW06818.

(RHON) RHONE POULENC RORER PHARM INC.

95US-00472964. 86US-00835594. 87US-00134499. 91US-00693079. 94US-00334884. 91US-00799859.

07-JUN-1995; 03-MAR-1986; 27-NOV-1991; 03-NOV-1994:

18-DEC-1987; 29-APR-1991;

1. .507 /*tag=

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US5571790-A. 05-NOV-1996

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flanking regions sequenced by the chain termination method. DNA sequences (see also AAT45983-84) derived from the complete cDNA can be used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 TIATACGGCTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAAC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                        large-scale prodn. of recombinant ECGF beta (AAM06816) and alpha (AAM06817) in transformed host cells. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
Recombinant human endothelial cell growth factors - for treating damaged
                                                                                                                                                                      A cDNA clone (AAT45985) codes for human endothelial cell growth factor (AAM66818). To obtain the clone, a human brain stem cDNA library was screened with a probe (see also AA45986) based on N-terminal sequences of bovine ECGF (see also AAW06819-20). ECGF clones 1 and 29 were isolated, subcloned into M13mp8 and the ECGF open reading frame and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GGGACAAGGACGGACCGACCACATTCAGCTGCAGCTGCGGAAAGGGTGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 GAGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGACGGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAATTCGGGAACGCGCCACAAGCAGCAGCTGCTGAGGCCATG-GCTGAAGGGGAAATCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 TTATACGGCTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.5%; Score 622.2; DB 2; Length 639; 99.4%; Pred. No. 9.3e-183; ative 0; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 639 BP; 172 A; 165 C; 168 G; 134 T; 0 U; 0 Other;
                                                                                                             Example D; Fig 8; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               635; Conservative
                                     blood vessels, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF field.)
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This invention relates to a combination comprising several cDNAs that are differentially expressed in activated vascular tissue. The invention also discloses a high throughput method for detecting differentially expressed cDNAs in a sample. The cDNAs of the invention may have antiatteriosclerotic, cytostatic, cardiant, hypotensive, antidiabetic; gynaecological, vasotropic and exebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a high-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page; 18pp; English.
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AGITICGAGGGGTCCTCACCTGGTTGACCCCAAAAATGTTCCCTTGACCATTGGCTGCGC 599
              Composition useful for identifying modulators of fibroblast growth factor -mediated signaling for use in treating cancer, has ternary complex of FGF-receptor, FGF ligand and heparin agonist or antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 TTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 ITCACAGACCCTGACGAGAAGTITAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 CTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 CTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 ACAAGGGACAGGAGCGACCAGCACTTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGAG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ATTCGGGAACGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to an isolated composition comprising a ternary complex of an Fibroblast Growth Factor (FGF) ligand polypeptide (ABR56163, ABR56165), an FGF receptor polypeptide (ABR56164) and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heparin agonist or antagonist, where the agonist or antagonist binds to
the FGF ligand polypeptide and the FGF receptor polypeptide to form the
ternary complex. The composition is useful for identifying a compound
that is an inhibitor of FGF receptor activity. FGF1 is also known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                        ds.
                                                                                                                                                                                                                                                                       Human, Fibroblast Growth Factor 1; FGF1; acidic FGF; aRGF; acidic Fibroblast Growth Factor; protein co-ordinate data; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2357 BP; 691 A; 521 C; 567 G; 578 T; 0 U; 0 Other;
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                                                      TAACCCCCAGGCCCAGAGCCTGAATTTGTAAGCAACTT 638
                                                                                  601 TAACCCCCAGCCCACAGAGCCTGAATTTGTAAGCAACTT 639
                                                                                                                                                                                                                                           Human Fibroblast Growth Factor 1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 16B; 288pp; English.
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          /product= "FGF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Linhard RJ;
                                                                                                                                                        ACC42968 standard; DNA; 2357 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2002; 2002WO-US034986.
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                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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286 ACAAGGGACAGGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGGG 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           542 TITICGAGGGGTCCTCACCTGGTTGACCCCCAAAAATGTTCCCTTGACCATTGGCTGCGCTA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           646 TITCGAGGGCCCTCACCTGGTTGA-CCCAAAATGTTCCCTTGACCATTGGCTGCGCTA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant; hypotensive; antidiabetic; gynaecological; vasctropic; cerebroprotective; gene therapy; vascular disease; cancer; coronary; artery disease; hypertension; diabetes; pre-eclampsia; restenosis; ischaemia-reperfusion injury; stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several CDNAs that are differentially expressed in activated
                                                                                                                                          346 GIGTATATAAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACGGACACGGGCTTTTA
                                                                                                                                                                                                                                                                                 406 TACGGCTCACAGACACCAAATGAGGGAATGTTTGTTCCTGGAAAGGCTGGAAGGAGGAACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               526 AATGGGAGCTGCAAACGCGGTCCTCGGACTCACTATGGCCAGAAAGCAATCTTGTTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA #225 differentially expressed in activated vascular tissue.
                                                                                                        243 GIGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGCTTTTTA
                                                                                                                                                                                                                                            303 TACGGCTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGGAACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      466 TACAACACCTATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGCCTCAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 AATGGGAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483 CCCTGCCAGTCTCTTCTGATTAAAGAGATCTGTTCT-GGTGTTGACCACTCCAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    586 CCCCTGCCAGICICITCIGAITAAAGAGAICIGIICIGGGIGIIGACCACICCAGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               705 ACCCCCAGCCCACAGAGCCTGAATTTGTAAGCAACTT 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602 ACCCCCAGGCCCACAGAGCCTGAATTTGTAAGCAACTT 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABX63225 standard; cDNA; 4087 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-2000; 2000US-0222469P.
08-JAN-2001; 2001US-0260483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JAN-2002; 2002US-00044090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-110597/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BAND/) BANDMAN O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2002137081-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bandman 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX63225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary artery disease, hypertension, diabetes, pre-eclampsia, ischaemia-reperfusion injury, restenosis, or stores. The CDNAs can also be used for large-scale genetic or gene expression analysis of several new nucleic acid molecules. Antibodies to the proteins encoded by the CDNAs are useful for of the protein. The present sequence represents a cDNA of the invention that is differentially expressed in activated vascular tissue. Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly from USPTO at invention. A protein encoded by the CDNA may be used to screen several molecules or compounds to identify a ligand that specifically binds to the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or recombinant protein from a sample. The nucleotides may be useful for diagnosing pre-pathologic disorders, and chronic or acute diseases associated with abnormalities in the expression, amount or distribution expression of one or more throughput methods for detecting differential expression of one or mor cDNAs in a sample, or screening several molecules or compounds to identify a molecule or compound that specifically binds a cDNA of the http.seqdata.uspto.gov/sequence.html?DocID=20020137081

(revised)

Sequence 4087 BP; 1164 A; 886 C; 959 G; 1078 T; 0 U; 0 Other;

182 470 AGTCTTGAAAGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACC 529 122 CICIACIGIAGCAACGGGGGCCACITICCIGAGGAICCTICCGGAIGGCACACIGGAIGGG 649 482 530 ITCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTC 589 183 ACAAGGGACAGGAGGGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGAG 242 ACAAGGGACCAGGGACCAGCACTTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGAG 709 243 GIGIAIAIAAAAGAGIACCGAGACIGGCCAGIACIIIGGCCAIGGACACCGACGGGCIIIIIA 302 GTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTA 769 TACGGCTCACAGACACCAAATGAAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCAT 362 830 TACAACACCTATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGCCTCAAGAAG 889 3 AITCGGGAACGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACC 62 TTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTC 423 AATGGGAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTCTC CCCCTGCCAGTCTCTTCTGATTAAAGAGATCTGTTCT-GGTGTTGACCACTCCAGAGAAG 950 CCCCTGCCAGTCTCTCTATAAAGAGATCTGTTCTGGGTGTTGACCACTCCAGAGAAG CTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGG Gaps 2; 94.3%; Score 601.8; DB 7; Length 4087; 7; Indels 602 ACCCCCAGCCCACAGAGCCTGAATTTGTAAGCAACTT 638 Pred. No. 4.9e-176; 0; Mismatches Best Local Similarity 98.6%; Matches 628; Conservative Query Match 63 123 900 710 303 363 483 q g δ à q ð g g 셤 ä ö à à 셤 à g ö d ò q ð

à g à 윉 à 임 ò 유 ò 셤 à g ₹ 셤 à 셤 ò 1069 ACCCCCAGCCCACAGAGCCTGAATTTGTAAGCAACTT 1105 AAN93088 standard; DNA; 638 BP. AAN93088;

362 414 422 474

294

482

AAN93088

XXX

also AAN93087 and AAN93089. (Updated on 25-MAR-2003 to correct PA field.) 243 GIGTATATAAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTA 302 535 CCCTGCCAGTCTCTTCTGATTAAAGAGATCTGTTCTGGGTGTTGACCACTCCAGAGAAG 594 295 GIGIAIAIAAAGAGIACCGAGACIGGCCAGIACIIGGCCAIGGACACCGACGGCIIIIIA 354 Recombinant DNA encoding new fibroblast growth factor analogues - useful e.g. for accelerating wound healing and to control neovascularisation. 115 TTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTC 235 ACAAGGGACAGGACCACACACATCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGAG 1175 CTCTACTICTAGCAACGAGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGAATGGG 303 TACGGCTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGAGAACCAT 355 TACGGCTCACAGACACCAAATGAGAGAATGTTTGTTCCTGGAAAGGCTGGAGGAGGAGCAT 415 TACAACACCTATATATCCAAGAAGCATGCAGAGAAATTGGTTTGTTGGCCTCAAGAAG 3 ATTOGGGAACGCCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACC 55 AGTCTTGAAAGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACC 63 TTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTC 123 CTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGG 183 ACAAGGGACAGGACGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGAG 423 AATGGGAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTCTC 475 AATGGGAGCTGCAAAACGCGGTCCTCGGACTCACTATGGCCAGAAAGCAATCTTTGTTTCTC 483 CCCCTGCCAGTCTTCTGATTAAAGAGATCTGTTCT-GGTGTTGACCACTCCAGAGAAG The sequence encodes human acidic fibroblast growth factor (aFGF). 2, /*tag= a /label= human acidic fibroblast growth factor 86.2%; Score 549.8; DB 1; Length 638; Sequence 638 BP; 170 A; 156 C; 168 G; 144 T; 0 U; 0 Other; 7; Indels Pred. No. 3e-160; 0; Mismatches Acidic fibroblast growth factor; ss. Location/Qualifiers Protter A; Disclosure; Fig 2; 44pp; English. Acidic fibroblast growth factor. 88EP-00306158. 87US-00070797. 98.5%; (first entry) (BIOU) BIOTECH RES INST. Matches 576; Conservative 91. .555 Fiddes JC, Abraham JA, WPI; 1989-009785/02. N-PSDB; AAN93087. Best Local Similarity Homo sapiens. 06-JUL-1988; 07-JUL-1987; 25-MAR-2003 25-JUN-1990 11-JAN-1989. mat peptide EP298723-A. Query Match

Gaps

CTCAGTGCGGAAAGCGTGGGGGGGGTGTATAAAGAGTACCGAGACTGGCCAGTACTTG Fiddes JC, Abraham JA; WPI; 1987-093786/13. Homo sapiens. factor (FGF) 11-SEP-1986; 12-SEP-1985; 30-MAY-1986; WO8701728-A. 16-DEC-1985; 26-MAR-1987. 219 279 339 408 468 459 AAN71029; 6 Query Match RESULT 12 FGF AAN71029 à 셤 à g ΩD à g à ð 셤 à à g ò ò Them the parameters of expression vectors. The pleasment retails the 17 phage gene 10 promoter and transcriptional terminator for expression of heterologous proteins e.g. basic fibroblast growth factor. The novelty of heterologous proteins e.g. basic fibroblast growth factor. The novelty of plasmid darives from the inclusion of the plasmid stability region of plasmid RPA. This region allows maintenance of the plasmid and prevents plasmid loss without the need for antibiotic resistance genes for selection and maintenance. The RPA par region comprises the genes for by. C. D and E. They are placed in the plasmid under control of the laco operator and laci(g) repressor. The novel plasmid can be used to express proteins of pharmaceutical, agricultural or biocatalytic interest without the use of antibiotics in the culture medium which, when present in trace amounts in final preparations, could lead to undesired side effects or antibiotic resistant microorganisms flourishing Expression plasmids contg. phage T7 promoter - and stabilising par region from plasmid RP4. 228 CHICCGGATGGCACAGTGGATGGGACAGGACAGGACGACCAGCACCATTCAGCTGCAG 287 99 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 158 168 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 227 159 CTTCCGGATGGCACAGTGGATGGGACAAGGGACAGGGGGCGACCAGCACATTCAGCTGCAG 218 Expression vector; I') phage; gene 10; promoter; heterologous; circular; transcriptional terminator; plasmid stability region; RP4; maintenance; plasmid loss; anthiotic resistance; selection; pharmaceutical; agricultural; biocatalysis; ds. This is the nucleotide sequence of a novel expression plasmid derived from the pET series of expression vectors. The plasmid retains the T7 39 ATGGCTGAAGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCA /*tag= a /note= "contains sequence derived from par region of Gaps Sequence 8501 BP; 1862 A; 2422 C; 2426 G; 1791 T; 0 U; 0 Other; 0; DB 2; Length 8501; Indels 4 Match 73.8%; Score 470.6; DB 2; Local Similarity 99.2%; Pred. No. 4.3e-135; 0; Mismatches Location/Qualifiers Claim 11; Page 14-19; 35pp; French. Novel expression plasmid pXL2435. AAT12907 standard; cDNA; 8501 BP. (RHON) RHONE POULENC RORER SA. 94FR-00011049. 95WO-FR001178 plasmid RP4" 6038. .8499 (first entry) Matches 473; Conservative Crouzet J; WPI; 1996-179946/18. 14-SEP-1995; misc_feature WO9608572-A1. 16-SEP-1994; 05-NOV-1996 21-MAR-1996. Cameron B, Synthetic. AAT12907; Query Match RESULT ò 셤 ò 임 à g ò

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288 CTCAGTGGGGAAAGCGTGGGGAGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTG 347
                                                                                     GCCATGGACACCGACGGCTTTTATACGGCTCACAGACACCAAATGAGGAATGTTGTTC 338
                                                                                                                                          CTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAAG 467
                                                                                                                                                                                                                                                                                                                                399 AATTGGTTTGTTGGCCTCAAGAAGGAATGGGAGCTGCAAACGCGGTCCTAAAACTCACTAT 458
                                                                                                                                                                                                                                                                                                                                                                    156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The N-terminal AA sequence of both acidic and basic bovine FGF are used to construct long probes to screen human and bovine genomic libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA sequences encoding mammalian fibroblast growth factors - useful in prodn. of pure factors for use in wound healing and tissue repair and of probe for tumour testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of partially synthetic gene for human acidic fibroblast growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes. Isolated sequences are used in vector construction etc. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCCAGAAAGCAATCTTGTTCTCCCCTGCCAGTCTTCTGATTAAAGAGATCTG 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCATGGCTGAAGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 481 BP; 133 A; 118 C; 129 G; 101 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wound healing; tissue repair; tumour probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to transform CV-1 cells for FGF prodn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Fig 9; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85US-00775521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86WO-US001879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85US-00809163.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIOT-) BIOTECHN RES PARTNE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAN71029 standard; DNA; 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 467; Conservative
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241 TGGCTATGGACGACGACGGCTTTTATACGGCTCACAGACACCAAATGAGGAATGTTTGT 300
                                                                                                                                                                                                                                                                                                        121 TCCTTCCGGATGCCACAGTGGATGGGACAAGGGACAGGGGGGCGACCAGCACTTCAGCTGC 180
                                                                                                                                                                         277 TGGCCATGGACACCGACGGCTTTTATACGGCTCACAGACACCAAATGAGGAATGTTTGT 336
                                                                                                                                                                                                                                                                          337 TCCTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGA 396
                                                                                                                                                                                                                                                                                                                                                                              397 AGAATTIGGITITGIITGGCCTCAAGAAGAAIGGGAGCTGCAAACGCGGGTCCTAAAACTCACT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*\text{tag=} \ x /note= "biffers from haFGF cDNA sequence of Jaye et al in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Partially synthetic nucleotide sequence encoding human acidic fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3. .5 /\epsilon tag= \nu /*tag= \nu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human acidic fibroblast growth factor; synthetic gene; lambda HAG-9.1; pAL12-haFGF; pAL13-haFGF; E. coli r3 promoter.
                                                                           217 AGCTCAGTGCGGAAAGCGTGGGGGGGTGTATAAAAGAGTACCGAGACTGGCCAGTACT
                                                                                                                            181 AGCTCAGTGCGGAAAGCGTGGGGGGGGGTGTATATAAAGAGTACCGAGACTGGCCAGTACT
457 ATGGCCAGAAAGCAATCTTGTTTTCTCCCCTGCCAGTCTTTTCTGATTAAAG 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "from genomic lambda HAG-9.1 clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (123. .158)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (195. .230)
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/note= "oligo 11"
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/note= "oligo 13"
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/note= "oligo 1"
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/note= "oligo 2"
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/note= "oligo 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAN90994 standard; DNA; 481 BP.
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/note= "Differs from haFGF cDNA sequence of Jaye et al in
which this base was C. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA constructs contg. R3 promoter from E. coli - having high strength and being insensitive to catabolite repression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is referred to in the spec. as both Figure 10 and Figure 11. The 5' portion of the gene was provided by genomic lambda HAG-9.1 clone. This portion encodes the 15 amino acids of the pro sequence along with the first 25 amino acids of the mature 'primary' form of hargp. The remainder was constructed from synthetic oligo- nucleotides designed so as to yield the same nucleotide sequence as that reported for hargp cDNA by Jaye et al with 2 exceptions. One (see FT) was designed to destroy the Nocl site spanning codon 67 and the other was designed as as to add HindIII and EcoRI cleavage sites following the TRA termination codon. Neither of these changes affects the amino acid sequence encoded. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a transcription initiation sequence; a second nuclectide sequence to terminate transcription; a third sequence comprising a ribosomal binding site and translation initiation codon operably linked to 13, a fourth sequence encoding a heterologous structural gene (eg AAN9994); a fifth sequence of an A-T rich oligomer; and a sixth sequence which is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthetic gene is inserted into pAL12 and pAL13 making pAL12-harGF and pAL13-harGF respectively. It is part of a construct comprising: a first nucleotide sequence comprising an E. coli 13 promoter operably linked to
                                                                                                              complement (267. .303)
                                                                                                                                                                                                   complement (304. .338)
                                                                                                                                                                                                                                                                                      complement (339. .374)
                                                                                                                                                                                                                                                                                                                                                                         complement (375. .410)
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                                                                                                                                        note= "oligo 15"
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'note= "oligo 16"
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note= "oligo 17"
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/note= "oligo 19"
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/note= "oligo 10"
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/note= "oligo 20"
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/note= "oligo 5"
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'note= "oligo 6"
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/note= "oligo 7"
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/note= "oligo 8"
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'note= "oligo 9"
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which this base was G.

mutation

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operator sequence to regulate expression of the fourth sequence. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  301 TCCTGGAAAGGCTGGAGAGAACCATTACAACACCTATATATTCCAAGAAGCATGCAGAGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 AGAATTIGGTTTIGTTIGGCCTCAAGAAGAATGGGAGCTGCAAAACGCGGTCCTAAAACTCACT 456
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                                                                                                                                                           1 CCATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTC
                                                                                                                                                                                                           61 CAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTCAGGA
                                                                                                                                                                                                                                                     157 TCCTTCCGGATGGCACAGTGGATGGGACAAGGGACAGGAGCGACCAGCACCATTCAGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 ATGGCCAGAAAGCAATCTTGTTTCTCCCCCTGCCAGTCTCTTCTGATTGAAG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       457 ATGGCCAGAAAGCAATCTTGTTTCTCCCCCTGCCAGTCTCTTGTTAAAG 508
                                                                                                      ·,
                                                                        Length 481;
                                           Sequence 481 BP; 133 A; 118 C; 129 G; 101 T; 0 U; 0 Other;
                                                                                                    5; Indels
                                                                        Score 464; DB 1; I
Pred. No. 1.2e-133;
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29-NOV-2001; 2001DB-01058411.
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                                                                                    al Similarity 98.9%;
467; Conservative
                                                                        72.7%;
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                                                                                      Local Similarity
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                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 CTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGAAG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 AATTGGTTTGTTGGCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCTCGGACTCACTAT 420
                The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNAI) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (as1) of dsRNA1 is complementary to (I) and at least part of one strand has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. in humans, also genes in plasmodium or in viruses or viroids that are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Double stranded RNA; dsRNA; RNAI; RNA inhibition; cytostatic; virucide; profozoacide; gene expression; antisense; tumour; infection; Plasmodium; virus; viroid; anti-tepp; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
                                                                                                                                                                   pathogenic for humans, animals or plants. Introducing an overhang into daRMA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399 AATTGGTTTGTTGGCCTCAAGAATGGGAGCTGCAAACGCGGCTCTAAAACTCACTAT
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             39 ATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 CTTCCGGATGGCACAGTGGATGGGACAAGGGACAGGAGGGACCAGCACCATTCAGCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CTTCCGGATGGCACAGTGGATGGGACAAGGGACGAGCGACCAGCACATTCAGCTGCAG
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0
                                                                                                                                                                                                                                                                                                                                      72.6%; Score 463.2; DB 6; Length 468; 99.4%; Pred. No. 2.2e-133;
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                                                                                                                                                                                                                                                                                               Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                     a gene related to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABZ35755 standard; DNA; 468 BP.
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                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonucleotides (dsRNAI and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (31, 22) of the ds structures in each of dsRNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAi). The method is particularly used to treat tumours or infections, especially by Plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCAGTGCGGAAAAGCGTGGGGGGGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTG 240
                                                            Inhibiting expression of target genes, useful e.g. for treating tumors, by introducing into cells two double-stranded RNAs that are complementary
                                                                                                                                                                                                                                                                                           and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 158
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4214.984 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
             Kreutzer R, Limmer S, Rost S, Hadwiger P;
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Job time : 444 sers
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                                                                                                               Claim 13; Page 44; 100pp; German.
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                                   WPI; 2002-683450/74.
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                                                                                      to the target.
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Sequence 3, Appli
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Patent No. 5437995
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Sequence 4, Appli
Patent No. 5514566
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Patent No. 5464943
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                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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0y 303 TACGOCTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCAT 362	0y 363 TACAACACCTATATATCCAAGAAGCATCCAAGAAGATTGCTTTGTTGGCCTCAAGAAG 422	0y 423 ARIGGGAGCTGCAAAGGCGCCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTCTC 482	Qy 483 CCCCTGCCAGTCTCTTCTGATTAAAGAGATCTGTTCT-GGTGTTGACCACTCCAGAGAAG 541	Oy 542 TITICGAGGGGCTCCTCACCTGGTTGACCCCAAAATGTTCCCTTGA 586	RESULT 2	US-09-023-655-1190 ; Sequence 1390, Application US/09023655 ; Patent No. 6607879	; GENERAL INFORMATION: ; APPLICANT: Cocks, Benjamin G. . abplicant: Sinsan G. Sinsart	至	; TITLE OF INVENTION: EXPRESSION ; NUMBER OF SEQUENCES: 1508	CORRESPONDENCE ALUKESS: - CORRESPONDENCE PHARMACEUTICALS, INC.	SIKERI: 31/4 FOKIEK DKIVE ; CITY PALO ALTO CHANGE ANT TROUBLE	- 52 6	COMPUTER READDABLE FORM: , MEDIUM TYPE: Ploppy disk	COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS	; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 ; CURRENT APPLICATION DATA:	FILING DATE: HEREWIN	CLASSIFICATION: ; PRIOR APPLICATION DATA: . add: add: add: add: add: add: add: add		ATTORNEY/AGENT INFORMATI NAME: Zeller, Karen J	REGISTRATION NUMBER: 37,071 ; REFERENCE/DOCKET NUMBER: PA-001 US : TELECOMMUNICATION INPOSANTION:		; INFORMATION FOR SEQ ID NO: 1390: ; SEQUENCE CHARACTERISTICS:	; LENGTH: 490 base pairs ; TYPE: nucleic acid	; STRANDEDNESS: single ; TOPOLOGY: linear . TAMPIATE SCHIPTE.	; LIBRAKY: GENBANK ; CLANE: a396163	Query Match 76.1%; Score 485.2; DB 4; Length 490; Best Local Similarity 99.4%; Pred. No. 1.3e-145; Matches 487; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Qy 29 CTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTCACAGCCGGGGAGAGTTTAA 88
ALIGNMENTS		sequence 3, Apr Patent No. 6294 GENERAL INFORM APPLICANT:	; APPLICANT: ARRAHAM, J.D. ; TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH ; TITLE OF INVENTION: FACTOR ANALOG ; NUMBER OF SEQUENCES: 69	CORRESPOND ADDRESSE STREET: CITY: F	; STATE: CA ; COMMIRY: USA ; ZIP: 94304-1018	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Diskette ; COMPUTER: IBM Compatible	0 1	; CURKENI AFPLICATION LAIA: ; APPLICATION NUMBER: US/09/098,628 ; FILING DATE:	ł4		; ATTORNEY/AGENT INFORMATION: ; NAME: Lehnhardt, Susan K		; TELEPHONE: TELEPHONE; TELEPHONE	2 2	; SEQUENCE CHARACTERISTICS: ; LENGTH: 638 base pairs	; TYPE: nucleic acid ; STRANDEDNESS: double	; TOPOLOGY: linear ; MOLECULE TYPE: CDNA	; realows: Coding Sequence; LoCallon: 91555	; OTHER INFORMATION: US-09-098-628-3	Query Match 86.2%; Score 549.8; DB 3; Length 638;	rative 0; Mismatches	Qy 3 ATTCGGGAACGCCACAAGCAGCAGCTGCTGAGCGTGAGGGGAAATCACCACC 62	Db 55 AGTCTTGAAAGCGCCACAAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACC 114	Qy 63 TTCACAGCCCTGACCGAGAGTTTAATCTGCCTCCAGGGAATTACAAGAACTC 122 [1.13 ILCACAGCCCIGACCGAGAGGIIAAICIICACCCLCAGGGGAAIIACAAGAGAGCCCAGAGACCCCAGAGACACAGAGAGAG		

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TRCARCACTATATATCCAAGAAGCATGCAGAGAATTGGTTTGTTT	aatgggagctgcaaacgcggtcctaaaactcactatggccagaaagcaatcttgtttctc 	CCCTGCAGTCTCTCTGATTAAAGAGATCTGTTCT-GGTGTTGACCACTCCAGAGAAG 	FGA 586 GA 638	0P BLOOD	Length	CTECTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGACAAGTTTAA 	TCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTT
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TACAAC TACAAC	AATGGG AATGGG		TTTCG# TTTCG#	No. 6678-1390 P. 1390, Application No. 667879 AL INFORMATION: LICANT: Cocks, Ben. LICANT: Susan G. S. LICANT: Susan G. S. LICANT: JECKT: SUSAN G. LICANT: JECKT: SUSAN G. LE OF INVENTION: C. LE OF INVENTIO	ë.		
363	423	483	542	ULT 2 19-023-655-1390 Gequence 1390, Application US/ GEMERAL INFORMATION: APPLICANT: Susan G. Stuart APPLICANTON: COMPORTER UNDERSORE: 1508 COMPUTER: 1214 PORTER DRIV COMPUTER: PALO ALTO STATE: A104 COMPUTER: EADABLE FORM: MEDIUM TYPE: P.C.DOS SOFTWARE: Word Perfect G. COMPUTER: EADABLE FORM: MEDIUM TYPE: P.C.DOS SOFTWARE: MORD PERFORM COMPUTER: BER PC COMPATA: APPLICATION NUMBER: US/O FILING DATE: FLING DATE: CLASSIFICATION: PRIOR APPLICATION REGISTRATION: REGISTRATION	atch cal 48	29	8
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                                                                                                                                                      108 ATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCA 167
                                                                                                                                                                                                       99 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGCCACTTCCTGAGGATC 158
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                                                      0; Gaps
73.8%; Score 470.6; DB 3; Length 8501; 99.2%; Pred. No. 2.8e-140; Live 0; Mismatches 4; Indels 0;
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APPLICANT: Chernykh, Svitlana I.

APPLICANT: Chernykh, Svitlana I.

APPLICANT: Slavchenko, Iryna Yu.

APPLICANT: Vozianov, Oleksandr

TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT

TITLE OF INVENTION: PIRROBLAST GROWTH FACTOR 155

FILE REFERENCE: CVGENG, 008A

CURRENT APPLICATION NUMBER: US/09/929, 945

VURRENT PILING DATE: 2001-08-15

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FRASESQ for Windows Version 4.0
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; Patent No. 6642026
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; APPLICANT: Stegmann, Thomas
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        Query Match
Best Local Similarity 99.2%
Matches 473; Conservative
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IITLE OF INVENTION: ACID-RESISTANT FGF COMPOSITION AND METHOD
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FILING DATE: 20-UUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 234,966
FILING DATE: 19-AUG-1988
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Best Local Similarity
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;Patent No. 5437995
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TITLE OF INVENTION: MONOCLONAL ANIBODY AGAINST AN ACIDIC

FGF PROTEIN AND HYBRIDOMA FOR ITS PRODUCTION

APPLICATION NUMBER: US/08/26,257 FILING DATE: 04-MAR-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: 588,343 FILING DATE: 26-SEP-1990

LENGTH: 450

5437995-1

SEQ ID NO:1:

NUMBER OF SEQUENCES: 3 CURRENT APPLICATION DATA:

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190
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                                                                                                                                                                                                                                                                                                                       124 CAGGA-CGACCACCACTTCAGCTGCAACTCAGTGCGGAAAGCGTGGGGGGAGGTGTATAT 182
                                                                                                                                                                                                                                                                                                                                                                                        311 ACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGCAACCATTACAACAC 370
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                                                                                                                                                                                                             64 CAGCAACGGGGCCACTTCCTGAGGATTCTTCCGGATGGCACAGTGGATGGGACAAGGGA
                                                                                                                                                                                  131 TAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACGGGGTGGGATGGGACAAGGGA
                                                                                           71 CCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCCAAACTCCTTACTG
                                                                                                                                    4 crraccreccargithaarcreccreceggaarracaagaageecaaacrecrerere
                                                  4;
    DB 6; Length 450;
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APPLICANT: Baird, J. Andrew
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6300 Columbia Center, 701 Fifth Avenue
56.7%; Score 361.6; DB 6; 94.8%; Pred. No. 4.9e-106; Live 0; Mismatches 19;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: No. 6083706tenburg Ph.D., Carol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatil
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                                                417; Conservative
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                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                               56.1%; Score 357.8; DB 4; Length 454;
91.5%; Pred. No. 8.2e-105;
tive 0; Mismatches 17; Indels 23; Gaps
                                                                                                                                                                                        Indels 23; Gaps
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APPLICANT: Andrew Baird
APPLICANT: Andrew Baird
APPLICANT: Dale E. Warnock
TITLE OF INVENTION: MODULANCES OF LEADERLESS PROTEIN EXPORT
TITLE OF INVENTION: AND METHODS FOR IDENTIFYING AND USING THE SAME
FILE REPERENCE: 2001244.02C4
CURRENT APPLICATION NUMBER: US/09/451,905
CURRENT FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                      56.1%; Score 357.8; DB 3; Length 454; 91.5%; Pred. No. 8.2e-105; tive 0; Mismatches 17; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09451905
Patent No. 6306613
          TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 91.59
Matches 431, Conservative
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US-09-451-905-14
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                             TOPOLOGY: linear
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120 ATATGTTTAACCTTCCGCCCGGGAATTACAAAAAACCCCAAGCTTCTTTACTGCAGTAACG 179
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139 GGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGGACAAGGGACAGGAGGG 198
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                                                                 399 AATTGGTTTGTTGGCCTCAAGAATGGGAGCTGCAAAACGCGGTCCTAAAACTCACTAT 458
                                                                                                             482 AACTGGTTTGTAGGCCTTAAAAAATGGTTCCTGTAAGCGTGGACCACGGACTCACTAT 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Chemically synthesized sequence for human acidic OTHER INFORMATION: Fibroblast Growth Factor (140 amino acids) using OTHER INFORMATION: preferred codons for E. coli
                                                                                                                                                        459 GGCCAGAAAGCAATCTTGTTTCTCCCCTGCCAGTCTCTTCTGATTAAAGA 509
                                                                                                                                                                             Score 280.6; DB 4; Length 630;
Pred. No. 5.4e-80;
0; Mismatches 94; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Slavchenko, Iryna Yu.
APPLICANT: Vozianov, Oleksandr
TITLE ORIVENTION: SUPER PRODUCTION OF RECOMBINANT
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: CVGENG.008A
CURRENT APPLICATION NUMBER: US/09/929,945
                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09929945
Patent No. 6642026
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  Kordyum, Vitaliy A.
Chernykh, Svitlana I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.0%;
78.2%;
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Stegmann, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             499 CTGATTAAAGA 509
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LOCATION: (122)...(544)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              630
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                                                                                                                                                                                                                                                                                           -09-929-945-6
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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RESULT 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 TIGGITIGITIGGCCTCAAGAAGGAATGGGAGCTGCAAACGCGGGTCCTAAAACTCACTATGG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 GAATTACAAAAACCCAAGCTTCTTTACTGCAGTAACGGAGGACACTTCCTGCGAATTCT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 CTCGGCCGAAAGCGTTGGAGAGGTCTATATCAAGTCGACGGAGACTGGCCAGTACCTTGC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 GGAAAGGCTGGAGGACAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGAAGAA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 CTGGTTTGTAGGCCTTAAAAAAATGGTTCCTGTAAGCGTGGACCCACGGACTCACTATGG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 GAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 TCCGGATGGCACAGTGGATGGGACAAGGACAGGAGCGACCAGCACTTCAGCTGCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 GCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGACCAGCACATTCAGCTGCAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Chemically synthesized sequence for human acidic OTHER INFORMATION: Fibroblast Growth Factor (134 amino acids) using OTHER INFORMATION: preferred codons for E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461 CCAGAAAGCAATCTTGTTTCTCCCCCTGCCAGTCTCTTTCTGATTAAAGA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.0%; Score 268.2; DB 4; Length 630; 78.5%; Pred. No. 5.1e-76; tive 0; Mismatches 88; Indels 0;
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                                                                                                                                                                                                       TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT TITLE OF INVENTION: PIBROBLAST GROWTH FACTOR 155
                                                                                                                                                                                                                                                    PILE REPERENCE: CYGENG.008A
CURRENT APPLICATION NUMBER: US/09/929,945
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
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FILING DATE: 0-S-ARK-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 809,163
; Sequence 4, Application US/09929945
; Patent No. 6642026
                                                                                                      APPLICANT: Kordyum, Vitaliy A.
APPLICANT: Chernykh, Svitlana I.
APPLICANT: Slavchenko, Iryna Yu.
APPLICANT: Vozianov, Oleksandr
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FILING DATE: 12-SEP-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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CURRENT APPLICATION DATA:
                                                                              APPLICANT: Stegmann, Thomas
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Matches 321; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (122)...(526)
                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 630
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                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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US-09-929-945-4

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27.4%; Score 174.8; DB 6; Length 197;
98.9%; Pred. No. 2.3e-46;
Live 0; Mismatches 2; Indels 0; Gaps 0;
                                                                                                                                                           96 CCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGG 155
                                                                                                                                                                                67 CCAGGGAATIRCAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGG 126
                                                                             36 GCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCT 95
                                                                                                       7 GCCAIGGCTGAAGGGGAAAICACCACCTICACAGCCCTGACCGAGAAGTTTAAICTGCCT 66
                                                                                                                                                                                                                                        156 AICCTTCCGGATGGCACAGTGGATGGGACAAGGGACGGAGCGACCAGCACATTCAGC 213
                                                                                                                                                                                                                                                              APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
ITILE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREEF: 22052 Davis Medical Research Center, 480 West
STREET: 9th Avenue
CITY: Columbus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL: J. Biol. Chem.
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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ORGANISM: No. 5750365ophthalmus viridescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/070,165F
                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08070165F
Patent No. 5750365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patrie, Kevin M
Botelho, Mary Jane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1. SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ray, Subir K
Mehta, Veela B
Chiu, Ing-Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                    Matches 176; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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PUBLICATION INFORMATION:
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MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE TYPE: Brain
                 Best Local Similarity
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POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                             US-08-070-165F-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS:
Query Match
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0; Mismatches 60; Indels

Matches 201; Conservative

0; Gaps

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GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
                                                                                                                                                                                                                                                                                ADDRESSEE: Ing-Ming Chiu
STREET: S2052 Davis Medical Research Center, 480 West
STREET: 9th Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: No. 5925528ophthalmus viridescens
DEVELOPMENTAL STAGE: Adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/885,418
330 TGITTGITCCTGGAAAGGCTG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                      241 TGCCTGTTCTTGGAGCGACTG 261
                                                                                                                               ; Sequence 1, Application US/08885418
; Patent No. 5925528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEPAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Botelho, Mary Jane
Ray, Subir K
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Chiu, Ing-Ming
J. Biol. Chem.
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PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE: Brain
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CLONE: MP 75-1
POSITION IN GENOME:
UNITS: bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGIE TYPE: CD
                                                                                                                                                                                                                                                                                                                                         CITY: Columbus
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: NO. 5
                                                                                                                                                                                                                                                                                                                                                                               USA
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LOCATION: 1...2
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                                                                                          RESULT 14
US-08-885-418-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS:
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25.9%; Score 165; DB 1; Length 261; 77.0%; Pred. No. 3.8e-43;

Best Local Similarity

Query Match

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RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 261
    ; RELEVANI
US-08-885-418-1
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6501.952 Million cell updates/sec

1 gaattcgggaacgcgccaca......cctgaatttgtaagcaactt 638

US-10-022-554A-3

Perfect score:

Sequence:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Listing first 45 summaries

Database :

Maximum Match 100%

3228839 seqs, 2456066551 residues

Searched:

Gapop 10.0 , Gapext 1.0

IDENTITY NUC

Scoring table:

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90 CTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTATACTAGCAACGGGGGCCACTTC 149
                                                                                                                                         150 CTGAGGATCCTTCCGGATGGCACAGTGGGACAAGGGACAGGAGCGACCAGCACTT 209
                                                                                                                                                                   269
                                                                                                                                                                                                                                                                                     270 CAGTACITIGGCCAIGGACACCGACGGCTITITATACGGCTCACAGACACCAAATGAGGAA 329
                                                                                                                                                                                                                                                                                                                        181 CAGTACTTGGCGATGGACGGCGACGGCAGTTATACGCATCTCAATCACCAAGCGAGGAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               o;
                                                                                                      1 CITCCCAATGGAAACTACCAGAAGCCTAAAGCTCCTGTACTGCAGCAACGGAAGGTACTTC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 TAACCTGCGCAATTACAAGAAGCCCAAGCTCCTCTACTGCAGCACGGGGGGCTA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 CTICCTGAGGATCCTTCCGGATGGCACAGTGGATGGGACAAGGGACAGGAGGGACCAGCA 205
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                                          Gaps
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     Length 261;
                                      60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; APPLICANT: FIDDES, JOHN C.; ABRAHAM, JUDITH A.; TITLE OF INVENTION: METHODS OF PRODUCING RECOMBINANT; FIBROBLASTS GROWTH FACTORS
25.9%; Score 165; DB 2; 77.0%; Pred. No. 3.8e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compug
                                  0; Mismatches
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FILING DATE: 05-ARR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             330 TGTTTGTTCCTGGAAAGGCTG 350
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FILING DATE: 16-DEC-1985
APPLICATION NUMBER: 775,521
FILING DATE: 12-SEP-1985
                                Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Patent No. 5514566
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

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10: 11: 12: 12: 13: 14: 16: 17: 17:

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Sequence 10, Appl
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Sequence 14, Appl
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Sequence 29943, A
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US-09-968-007A-440
               US-10-044-090-225
US-09-902-460-3
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US-09-929-945-6
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US-10-649-480-4
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August 24, 2004, 18:53:06 ; Search time 482 Seconds

OM nucleic - nucleic search, using sw model

Run on:

Compugen Ltd.

(without alignments)

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Sequence 6, Appli Sequence 6, Appli Sequence 1, Appli	Sequence 26, Appl Sequence 700, App Sequence 114, App	Sequence 3, Appli Sequence 3, Appli	Sequence 11, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 4, Appli Sequence 13, Appl	Sequence 15, Appl
15	10 US-09-775-964-26 15 US-10-311-455-700 17 US-10-433-793-114	9 US-09-802-365-3 9 US-09-886-856-3	15 US-10-155-785-11 9 US-09-802-365-7			13 US-10-408-415-4	9 US-09-934-706-15
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Qy 542 TITCGAGGGTCCTCACTGGTTGACCCGAAAATGTTCCCTTGACCATTGGCTGCGTA 601	Oy 602 ACCCCAGCACAGAGCCTGAATTTGTAAGCAACTT 638 	RESULT 2 US-09-902-460-3 ; Sequence 3, Application US/09902460 ; Publication No. US2003004004241 ; GENERAL INFORMATION: ; ARRAPALIANCEMATION: ; APPLICANT: FIDDES, J.C. ; TITLE OF INVENTION: HAMAN BASIC PIBRORIAST CROWTH	G TER TER WS Version 02,460	FILING DATE: CURKHOWN: ATTORNEY/AGENT INFORMATION: NAME: Lethnhardt, 33.943 REFERENCE/DOCKET UNBER: 21900-20089.10 TELEFONNE 650-813-5600 TELEFONNE 650-494-0792 TELEFONNE 650-494-0792 TELEFONNE CHARACTERISTICS: CO-494-0792 INFORMATION FOR SED ID No. 3: SEQUENCE CHARACTERISTICS: LONG INFORMATION FOR SED ID No. 3: SEQUENCE CHARACTERISTICS: LONG TELEFONNE CHARACTERISTICS: CO-494-0792 INFORMATION FOR SED ID No. 3: SEQUENCE CHARACTERISTICS: LONG TYPE: nucleic acid STRANDENNESS: double TYPE: CO-400-400-400-400-400-400-400-400-400-40	Db 175 CICIACIGIAGCAACGGGGCCACTICCTGAGGATCCTTCCGGATGGCACAGTGGGATGGG 234
18.8 1374 10 US-U99-991-1 18.8 16602 15 US-10-311-455-700 18.8 18357 17 US-10-311-455-71 18.8 18357 17 US-10-433-793-114 18.7 44.1 9 US-08-802-865-3	119.2 18.7 441 9 US-09-886-856-3 119.2 18.7 444 15 US-10-155-785-11 119.2 18.7 474 9 US-09-802-365-7 119.2 18.7 474 9 US-09-886-856-7 119.2 18.7 489 9 IN-09-844-766-11	18.7 489 13 18.7 489 13 18.7 1182 13 18.7 1527 9	RESULT 1 US-10-044-090-225 Sequence 225, Application US/10044090 Publication No. US20020137081A1 GENERAL INFORMATION: APPLICATION NO. US20020137081A1 TILLE OF INVENTION GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION TILLE OF INVENTION DATE: 2002-01-09 CURRENT PILING DATE: 2002-01-09 NUMBER OF SEQ ID NOS: 850 SOFTWARE: PER PROGram SOFTWARE: PRA 4087 TYPE: DNA GRGANISM: Homo sapiens FEATURE: NUMBER (MYSTER) NO SAPIENS GRGANISM: Homo sapiens SEATURE: NUMBER (MYSTER) MYSTER) US-10-044-090-225	Query Match 94.3%; Score 601.8; DB 14; Length 4087;	

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18; Score 549.8; DB 10; Length 638;
18; Pred. No. 6e-175;
0; Mismatches 7; Indels 2; Gaps 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGGCCACITICCTGAGGATCCITICGGATGGCACAGTGGATGGG 182
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HUMAN BASIC FIBROBLAST GROWIH
FACTOR ANALOG
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: DATA:
MBER: US(09/902,460
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THROWATION:

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Db 301 ATGTTTGTTCCTGGAAAGGTGGAACCATTACAACACCTATATATCCAAGAAGCA 360 Oy 389 TGCAGAGAAATTGGTTTGTTGGCCTCAAGAAAGGAGCAAACGCGAACGGGTCCTTA 448	RESULT 4 US-10-641-643-1390 ; Sequence 1390, Application US/10641643 ; Publication No. US20040077003A1 ; GENERAL INFORMATION; Susan G. Stuart ; Jeffrey J. Seilhamer ; Jeffrey J. Seilhamer ; TITLE OF INVENTION: CORPOSITION FOR THE DETECTION OF BLOOD CELL ; CORRESPONDENCES, 1508 ; CORRESPONDENCES, 1508	### ADDRESSER: INCITE PRABMACEUTICALS, INC. STREET: J174 PORTER DRIVE CUTTY FALO ALTO STREET: CALIFORNIA COMPUTER RADABLE FORM: ### COMPUTER INCITES INCOMPUTER INC. COMPUTER INCIDENCE INCOMPUTER INCOMPUTER INC. COMPUTER INCIDENCE INCOMPUTER INCOMPUTER INC. COMPUTER INCIDENCE INCIDENCE INCIDENCE COMPUTER INCIDENCE INCIDENCE COMPUTER INCIDENCE INCIDENCE COMPUTER INCIDENCE INCIDENCE COMPUTER INCIDENCE INCIDENCE THING DATE: 14-ANG-2003 CLASSIFICATION MARKE: CIRCHOM MAKE: 22-11-2 - CARACATION MAKE: 23-11-2 - CARACATIO
QY 183 ACAAGGACAGGACCACACTTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGG 242 Db 235 ACAAGGACAGGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGG 294 QY 243 GTGTATATAAAGAGTACCGAGCACTTCAGCTGCAGCACTGGACCGGACGGGTTTTA 302 Db 295 GTGTATATAAAGAGTACCGAGCACTGATTCTTGGCCATGGACACCGACGGGCTTTTA 354 QY 303 TACGGCTCACACACACACACACAGAATGATTCTTCTCTCGAAAGCTGGAGGAACCAT 362 Db 355 TACGGCTCACACACACACACACAGAATGATTTGTTCTCTCGAAAGCTGGAGGAACCAT 314 QY 363 TACAACACCACACACACACACACACACACACACACACAC	Qy 423 AATGGGGAACGCGGTCCTAAAACTCACTATGGCCAGAAGCAATCTTGTTTCTC 482 Db 475 AATGGGAGCTGCAAACGCGACTCACTATGGCCAGAAAGCAATCTTGTTTCTC 534 Qy 483 CCCTGCCAGTCTCTTCTGATTAAAGAGATCTGTTCT-GGTGTTGACCACTCCAGAGAAG 541 Db 535 CCCTGCCAGTCTTCTGATTAAAGAGATCTGTTCTGGGTGTTGACCACTCCAGAGAAG 594 Qy 542 TTTCGAGGGGTCTCTTCTGATTAAAGAGATCTGTTCTGGGGTGTTGACCACTCCAGAGAAG 594 Qy 542 TTTCGAGGGGTCTCACTTGTTGATTAAAAATGTTCCTTGA 586 Db 595 TTTCGAGGGGTCCCCCTCGTTGAACAATGTTCCCTTGA 638 Db 595 TTTCGAGGGGTCCCCCCCCCAAAAATGTTCCCTTGA 638	Segura 1 Segura 2 Segura 2 Segura 2 Segura 3 Seg

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459 GGCCAGAAAGCAATCTTGTTTCTCCCCCTGCCAGTCTTTCTGATTAA 506
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                          209 TCAGCTGCAGCTCAGTGCGGAAAAGCGTGGGGGGGGGTGTATAAAAGAGTACCGAGACTGG 268
                                                                          269 CCAGTACTTGGCCATGGACACCGACGGCTTTTATACGGCTCACAGACACCAAATGAGGA 328
                                                                                               329 ATGITITGITCCTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGCA 388
                                                                                                                                                                             301 AIGITICITICABAAAGGCIGGAGGAGAACCAITACAACACCCTATATATCCAAGAAGCA 360
                                                                                                                                                                                                                    389 TGCAGAGAAGAATTGGTTTTGTTGGCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCTAA 448
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APPLICANT: Cherrykh, Svitlana I.
APPLICANT: Slavchenko, Iryna Yu.
APPLICANT: Slavchenko, Iryna Yu.
APPLICANT: Vozianov, Oleksandar
ITILE OF INVENTION: PHAGE-DEPRIDENT SUPER PRODUCTION OF
ITILE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
FILE REPERENCE: PHAGE-DEPRENCE: PROTEIN AND PEPTIDES
CURRENT APPLICATION NUMBER: US/09/929,918
CURRENT FILING DATE: 2001-08-15
FRICA PAPLICATION NUMBER: 09/318,288
FRICA PAPLICATION NUMBER: 09/318,288
FRICA FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 72.6%; Score 463.2; DB 9; Length 468; Best Local Similarity 99.4%; Pred. No. 1e-145; Matches 465; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ' Sequence 3, Application US/09929918
' Patent No. US20020090678A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kordyum, Vitaliy A. APPLICANT: Chernykh, Svitlana
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ORGANISM: Homo sapiens
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US-09-929-918-3
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APPLICANT: Slavchenko, Iryna Yu.
APPLICANT: Vozianov, Oleksanda T.
TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIBROBLAST GROWTH FACTOR 155
                  FILE REFERENCE: CVGENG.008A
CURRENT APPLICATION NUMBER: US/10/280,864
                                                                                                                           NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REPERRICE: CYGENG.008A
CURRENT APPLICATION NUMBER: US/10/649,480
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION UNPERS: 10/649,480
PRIOR FILING DATE: 2003-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                            CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US/09/929,945
PRIOR FILING DATE: 2001-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 3, Application US/10649480
; Publication No. US20040115769A1
; GENERAL INFORMATION:
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Best Local Similarity 99.49
Matches 465, Conservative
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APPLICANT: Kordyum, Vitaliy
APPLICANT: Chernykh, Svitla
                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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US-10-649-480-3
                                                                                                                                                                                              LENGTH: 468
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qa	19	GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 120
à a	159	CITCCGGATGGCACAGTGGATGGGACAGGACAGGACCAGCAGCACATTCAGCTGCAG 218
5 d	219	CTCAGTGCGGAAAGCGTGGGGGGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTG 278
y B	279	GCCATGGACACCGACGTTTTATACGGCTCACAGACACCAAATGAGGAATGTTTGTT
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QY Dp	459	!
RESULT 9 US-09-929 Sequence Patent GENERAL APPLIC APPLIC APPLIC TITLE TI	SEGULT 9 Sequence 1, Applicate Seguence 1, December 1000 of Septicant Septican	ESULT 9 Sequence 1, Application US/09929918 Sequence 1, Application US/09929918 Sequence 1, Application US/09929918 Sequence 1, Application US/09929918 Fatent No. US20020090678A1 Sequence 10 September
Query Best Match	Query Match Best Local Sir Matches 373;	49.2%; Score 314.2; DB 9; Length 630; Similarity 79.2%; Pred. No. 2.9e-95; 3; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
Š A	39 A 122 A	ATGGCTGAAGGGGAATGACGACCTTGACAGCCCTGACGGAGGATTAATCTGCCTCCA 98
ે દ	g	GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAAGGGGGCCACTTCCTGAGGATC 158
i à		GOMMATINGMANANCICANGCTICTITIACIUCAGTAACGAAGAACTTCCTGCGAATT 241 CTTCCCGATGGCACAGTGGAACAAGGAACAAGGAGGACCAGCACATCAGCTGCAG 218

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242 CTGCCAGATGGCACAGTAGATGGGACTCGCGATCGCTCCGACCAGCACTTCAGCTGCAA 301
                                    219 CTCAGTGCGGAAAGCGTGGGGGGGGTGTATAAAGAGTACCGAGACTGGCCAGTACTTG 278
                                                           362 GCCATGGACCGATGGGCTTCTGTATGGCTCACAGACGCTAACGAAGAATGCTTGTTT 421
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                                                                                                                                                                                                                                                                                                                        459 GGCCAGAAAGCAATCTTGTTTCTCCCCTGCCAGTCTCTTCTGATTAAAGA 509
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APPLICANT: Slavchenko, Iryna Yu.
APPLICANT: Vozianov, Oleksandr
TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155
FILE REFERENCE: CUERC, 0.08A
CURRENT APPLICATION NUMBER: US/09/929,945
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Stegmann, Thomas
APPLICANT: Kordyum, Vitaliy A.
APPLICANT: Chernykh, Svitlana I.
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LOCATION: (122)...(590)
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Ä	Db 482	AACIGGITTGTAGGCCTTAAAAAAATGGTTCCTGTAAGCGTGGACCACGGACTCACTAT 541
δŏ	y 459	GGCCAGAAAGCAAICITGTTTCTCCCCCTGCCAGTCTCTTCTGATTAAAGA 509
do	b 542	GGCCAAAAGGCTATCTTGTTCCTGCCACTACGAGGACTCCGACTAAGGA 592
RE US	RESULT 11 US-10-280-864-1 ; Sequence 1, A	SULT 11 -10-280-864-1 Sequence 1, Application US/10280864 Publication No. US20030054492A1
	GENERAL INFORMATION: APPLICANT: Stegmann	NRMATION: Stegmann, Thomas
	APPLICANT: APPLICANT:	Kordyum, Chernykh
٠. ٠.	APPLICANT: APPLICANT:	Slavchenko, Iryna Y
	TITLE OF IN	VENTION: SU
h 14	FILE REFERE CURRENT APP	FILE REFERENCE: CVGENG.008A CURRENT APPLICATION NUMBER: US/10/280.864
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٠. ٠.	PRIOR FILING DATE: 201 NUMBER OF SEQ ID NOS:	01-08-15 8
٠. ٠.	SOFTWARE: F	
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	ORGANISM:	ORGANISM: Artificial Sequence
	OTHER INFO	equence for
		Fibroblast Growth Factor (155 amino acids) preferred codons for E. coli
· · ·	NAME/KEY: LOCATION:	CDS 1,122) (590)
	Query Match Best Local Si Matches 373.	2%; Score 314.2; DB 15; Length 63 2%; Pred. No. 2.9e-95;
	,	constructive U; Mismatches 98; Indels U; Gaps U;
£ £	39 8 39 1 42 27 1	ATGGTTGAAGGGGAAATGACCACCTTCACAGCCCTGACGGAGAAGTTTAATCTGCCTCGA 98 ATGGCTTGAAGGGGAAAGGGAAAGGAAGAGAAGAAGAAAGA
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第 台		GOGARITACARANGCUCAAACTCCTCTACTGTACCAACGGGGGCCACTTCCTGACGATC 158 GGGAATTACAAAAACCGAAGCTTCTTTCTTTTTTTTTTT
δ	29	TTCCGGATGGCACAGTGGATGGGACAAGGGACGAGGACGACATTCAGTGCAGATT
qq	242 C	CTGCCAGATGGCACAGTAGATGGGATCGCGATCGCTCCGACCACACATTCAGCTGCAA 301
ò	219 C	CTCAGTGCGGAAAGCGTGGGGGGGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTG 278
C C	302 C	CICTOGGCCGAAAGCGITGGAGGTCTATATCAAGTCGACGGAGACTGGCCAGTACCTT 361
à	279 G	GCCAIGGACACCGACGGGTITIAIACGGCTCACAGACACCAAAIGAGGAAIGITIGIIC 338
g	362 G	GCCATGGACACCGATGGGCTCTGTATGGCTCACAGACGCCTAACGAAGAATGCTTTT 421
ò	339 GE	CTGGAAAGGCTGGAGAGAGCCATTACAACACCTATATATCCAAGAAGATGCAGAAAG 398
Д		CTAGAAAGACTAGAAGAAAACCATTACAACACGTACATATCGAAAAAACATGCAGAGAGG 481
ð.		AATTGGTTTGTGGCCTCAAGAAAAGGGAGCTGCAAACGCGGTCCTAAAACTCACTAT 458
d d		AACTGGTTTGTAGGCCTTAAAAAAAAAAGGTTCCTGTAAGCGTGGACCACGGACTCACTAT 541
S &	459 GC 459 GC 542 GC	GGCCAGAAGCAATCTTGTTTCTCCCCGGGGTCTCTCTGATTAAAGA 509 GGCCAAAAGCGAATCTTGTTTCTCCCCGGGTCTCTTCTGATTAAAGA 509 GGCCAAAAGCGTTCTTTCTTCTTCTTTCTTTTCTTTTCT
		CONTRACTION CONTRACTOR CONTRAGEN 292

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 CTCTCGGCCGAAAGCGTTGGAGAGGTCTATATCAAGTCGAGGAGACTGGCCAGTACCTT 361
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                                                                                                     APPLICANT: Kordyum, Vitaliy A.
APPLICANT: Chernykh, Svitlana I.
APPLICANT: Slavchenko, Iryna Yu.
APPLICANT: Slavchenko, Oleksandr
TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155
                                                                                                                                                                                                                                    FILE REFERENCE: CVGENG.008A
CURRENT APPLICATION NUMBER: US/10/649,480
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 10/649,480
PRIOR FILING DATE: 2003-03-27
                    Sequence 1, Application US/10649480
Publication No. US20040115769A1
                                                                                                                                                                                                                                                                                     2003-08-27
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                                                                                       APPLICANT: Stegmann, Thomas
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                                                                                                                                                                                                                                                                                CURRENT FILING DATE:
                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                    CENGIH: 630
US-10-649-480-1
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BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES

TITLE OF INVENTION: BIOLOGICALLY ACTIVE P FILE REFERENCE: PHAGE.006A CURRENT APPLICATION NUMBER: US/09/929,918

NUMBER OF SEQ ID NOS: 11 SOFTWARE: FastSEQ for Windows Version 4.0

CURRENT FILING DATE: 2001-08-15 PRIOR APPLICATION NUMBER: 09/318,288 PRIOR FILING DATE: 1999-05-25

OTHER INFORMATION: Chemically synthesized sequence for human OTHER INFORMATION: interferon alpha- 2b

; LOCATION: (320)...(784) US-09-929-918-10

(231)...(249)

NAME/KEY: promoter LOCATION: (231)...(NAME/KEY: CDS

ORGANISM: Artificial Sequence

LENGTH: 990 SEQ ID NO 10 TYPE: DNA FEATURE:

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APPLICANT: Edner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Usining Signature
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-11
CURRENT APPLICATION NUMBER: US/09/968,007A
FILE REPERIOR APPLICATION NUMBER: US/60/237,172
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                                                                                                                                                                                                                              380 GGGAATTACAAAAAACCCAAGCTTCTTTACTGCAGTAACGGAGACACTTCCTGCGAATT 439
                                                                                                                                       320 AIGGCIGAAGGGAAAICACCACCIITAACAGCGITAACGGAGAAAITIAACCIICCGGCC 379
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                                                                                       39 AIGGCIGAAGGGGAAAICACCACCIICACAGCCCIGACCGAGAAGIIIAAAICIGCCICCA 98
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                                                       0; Gaps
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                                                    Indels
                                                    98;
                         Pred. No. 3.6e-95;
0; Mismatches 98
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PRIOR APPLICATION NUMBER: US/60/237,173
PRIOR FILING DATE: 2000-10-02
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PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,294
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
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                           79.2%;
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; GENERAL INFORMATION:
                                             Matches 373; Conservative
Query Match
Best Local Similarity
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APPLICANT: SLAVCHENKO, ITYMA YU.
APPLICANT: Vozianov, Oleksandr
TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF

Chernykh, Svitlana I.

APPLICANT:

GENERAL INFORMATION: APPLICANT: Kordyum, Vitaliy A.

Sequence 10, Application US/09929918 Patent No. US20020090678A1

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414 CTCAAGAAGAATGGGAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATC 473
                                                                                                                    406 CTCAAGAAGAATGGGAACTGCAAACGCGGTCCTCGGACTCACTATGGCCAGAAAGCAATC 465
                                                                                                                                                          474 INGITICICCCCCGCCAGTCTCTTATAAAGAGATCTGTTCT-GGTGTTGACCACT 532
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                                                                                                                                                                                                                                                           (without alignments) 6696.686 Million cell updates/sec
                                                                                                                                                                             1 gaattcgggaacgcgccaca.....cctgaatttgtaagcaactt 638
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 200000000
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                                                                                                                                                                                             Ouery Match 47.5%; Score 302.8; DB 12; Length 3658; Best Local Similarity 96.0%; Pred. No. 4.8e-91; Matches 332; Conservative 0; Mismatches 12; Indels 2; Gaps
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CURRENT APPLICATION NUMBER: US/09/968,007A
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,172
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PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR PLING DATE: 2000-10-02
PRIOR PRICATION NUMBER: US/60/237, 173
PRIOR PILING DATE: 2000-10-02
PRIOR PELING DATE: 2000-10-02
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PRIOR PLING DATE: 2000-10-02
PRIOR PLING DATE: 2000-10-02
PRIOR PLING DATE: 2000-10-02
NUMBER: US/60/237, 316
NUMBER: OF SEQ ID NOS: 1001
PRIOR APPLICATION NUMBER: US/60/237,316
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 1001
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 440, Application US/09968007A
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Matches 332; Conservative
                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-968-007A-133
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                                                                                                       LENGTH: 3658
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                                                                                  SEQ ID NO 133
                                                                                                                          TYPE: DNA
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28: gb_gssl:* 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SUMMAKIES	£	BX444567	B1869731	B0067949	0.000 0.000	2002020	B1753845	BI598390	AI590078	BG706412	AI077609	AK035330	BI692283	87956865		•	BU627243	CG633840	CG565930	BB627624	A1663400 RF532970	BU840197	BF958824	BF442355	CG554707	CG629018	AA261582	CB773841	AW259195	BM364189	BI598882	AA594274	AI083919	R54255	AA015793	AA238828	BB629001	AW531286	CG613113	CG496943	OTTAINED IN	ALIGNRENIS	1173 bp ADULT BRAIN H MRNA sequence	m	es;	•
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æ	Query	94.3	0	σ	0 0		, , ,		80.2	9.87	9.89	68.1	1 99	0.00	60.49	63.3	63.0	62.9	60.4	60.4	55.8	55.6	51.5	51.3	50.3	49.7	49.6	47.2	46.8	45.8	45.7	44.0	43.7	43.0	6.24	41.9	41.2	.i o	38.7				BX444567 BX444567 Homo CSODN003YP16 : BX444567	.567.1 GI:3078C Sapiens (human)	Eukaryota, Metazoa, Maumalia, Eutheria, 1 (bases 1 to 1173 Li, W.B., Gruber, C.,	Full-length cDNA libraries
	Score	601.8	76	569.4	567	560 8	0 0	0.00	511.4	9.100	437.6	434.6	4.55.4	2.525	408.2	404	402.2	401.2	385.4	385.2	356	354.6	328.6	4.728	320.6	316.8	316.6	307.8	6	292.2	291.4	280.6	279		273 6	267.4	62.	3 5	1 0	246				EST. HOMO Sap.	Eukar Mamma 1 (ba	Full-
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Oy 543 TTGGAGGGGTCCTCACCTGGTTGACCCCAAAATGTTCCCTTGACCATTGGCTGAA 602	RESULT 3		http://image.llnl.gov Plate: LLAM12829 row: j column: 16 High quality sequence stop: 470. FEATURES I. 1057 / organism="Homo sapiens" / db_xref="taxk" // db_xref="ta	/lab_host="DHIOB" //lone lib="WHIM MGC_121" //note="Organ: brain; Vector: pCMV-SPORT6; Site 1: Not1; Site_2: BCORV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (BCORV site is edstroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note:	0 0 0 0 0 0 0 0 0 0
7	AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Email: cgapbe.remail.nih.gov Tissue Procurement: Arrayed by: The I.M.so. Contact inc. CONA Library Preparation: Life Technologies, Inc. CONA Library Preparation: Life Technologies, Inc. CONA Library Arrayed by: The I.M.s.G. E. Consortium (LIML) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be	X .	Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. ORIGIN Query Match 90.44; Score 576.8; DB 12; Length 832; Best Local Similarity 98.34; Pred. No. 1.4e-158; Matches 625; Conservative 0; Mismatches 7; Indels 4; Gaps 4;	QY 5 TOGGRANGGEOCCACAAGCAGCAGCAGCAGCAGCAGAAATCACCACCTT 64 Db 46 TCTTGAAAGCGCCACAAGCAGCTGCTGAGCCATGAGCAGAAATCACCACCTT 105 QY 65 CACAGCCCTGACCGAGAAGTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCT 124 Db 106 CACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCT 165 QY 125 CTACTGTAGCAAGGGGGCCCATCCTGAGGATCCTTCCGGATGGCACAGTGGATGGGATGGGATGGAACCTTCCAGATGGATG	

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345 GTGTATATAAAGAGTACCGAGACTGGCCATGGACACCGACGGCCTTTTA 404 303 TACGGCTCACAGACACCAAATGAGGAATGTTTGTTCTGGAAAGGCTGGAGGAGAACAT 362	584 540 644 704	EMBSOUT 4 BMB09005 LOCUS BMB09005 BMB09005 BMB09005 SWARNITION AGENCOURT_6617747 NIH_MGC_124 Homo sapiens cDNA clone INAGE:5734445 ACCESSION BMB09005.1 GI:19125828 DD GY VERSION BMB09005.1 GI:19125828	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS NHI-MCA PLEPI/Mac.nci.nih.gov/. TITLE JOURNAL Unpublished (1999)	Il. Inh. gov In. Inh. gov In vitrogen aration: Life Technologies, Inc. Pred by: The I.M.A.G.E. Consortium (LiML) In MGC clone distribution information can be In MGC clone distribution information can be In MGC clone distribution information can be In M.A.G.E. Consortium/LiML at: The A.G.E. Consortium/LiML at: Th	age 2'. Library 1s oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."	Query Match 88.9%; Score 567; DB 12; Length 1014; Best Local Similarity 97.0%; Pred. No. 1.2e-155; Matches 610; Conservative 0; Mismatches 15; Indels 4; Gaos 3;

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linear EST 25-SEP-2001
   B1753045
878 bp mRNA linear EST 25-SEP-200
603027526F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5197783 5',
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Small: cgapbs.r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIAL)
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Plate: LLAM11495 row: d column: 08
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5197783"
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                                                                                                               BI753845.1 GI:15745423
                                                                                                                                                                      Homo sapiens (human)
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                                                         mRNA sequence.
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BI753845
                                                                                 BI753845
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRv (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dr primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.5 kb, insert size trange 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019: Note:

81 ANTCITGAAAGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCAGCACC 140 TTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAA-CT 121 CCTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGG 181 201 CCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACGGGTGG 260 182 GACAAGGGACAGGGGCCACCAGTTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGA 241 261 GACAAGGGACAGGACCAGCACATTCAGCTGCAGTGAGTGCGGAAAGCGTGGGGGA 320 301 321 GGIGTALATAAAGAGTACCGAGCTGGCCAGTACTTGGCCATGGACACCGACGGCTTTT 380 linear EST 07-SEP-2001 3 ATTCGGGAACGCCCACAGGAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACC 62 302 ATACGGCTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAAACCA 361 362 TTACAACACCTATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGCCTCAAGAA 421 441 TIACAACACCTATATATCCAAGAAGCATGCAGAGAATCGGTTTGTAGGCCTCAAGAA 500 422 GAATGGGAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTCT 481 CCCCCTGCCAGTCTCTGATTAAAGAGATCTGTTCTGGTGTTGACCACTCCAGAGAAG 541 561 CCCCTGCCAGTCTCTTCTGATTAAAGAGATCTGTCTGGGTGTAGACCACTCCAGAGAAG 620 542 IITCGAGGGTCCTCACCTGGTTGACCCCAAAAATGTTCCCTTGACCATTGGCTGCGCTA 601 619 Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarxhini, Hominidae, Homo. 603250094F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5302030 5', 242 GGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTT Gaps National Institutes of Health, Mammalian Gene Collection (MGC) 3; 87.9%; Score 560.8; DB 12; Length 878; 18; Indels Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. 0; Mismatches 18; mRNA (Invitrogen). Research Gethis is a NIH_MGC Library." 602 ACCCCCAGCCCACAGAGCCTGAATT 626 680 ACCCCCAG-CCACAGAGCCTGAATT 703 821 bp NIH-MGC http://mgc.nci.nih.gov/. BIS98390.1 GI:15491329 96.68; Homo sapiens (human) Matches 604; Conservative (bases 1 to 821) Unpublished (1999) mRNA sequence. Similarity Homo sapiens BI598390 BI59839(63 Query Match 122 482 DEFINITION ORGANISM ACCESSION AUTHORS TITLE REFERENCE JOURNAL BI598390 KEYWORDS ORIGIN VERSION SOURCE LOCUS ò a à g g ð à a ò g à a à 셤 ð 셤 à 셤 g à ò 셤

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKBN)
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: 63 TICACAGCCCTGACCGAGAAGTITAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTC 122 173 174 TICACAGCCCTGACCGAGAAGTITAAICTGCCTCCAGGGAAITACAAGAAGCCCAAACTC 233 123 CTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGG 182 183 ACAAGGGACAGGAGCGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGAG 242 243 GTGTATATAAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTA 302 62 473 363 TACAACACCTATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGCCTCAAGAAG 422 474 TACAACACCTATATATCCAAGAAGCATGCAGAAGAAGAATTGGTTTGTTGGCCTCAAGAAG 533 482 483 CCCCTGCCAGTCTCTTCTGATTAAAGAGATCTCTT-GGTGTTGACCACTCCAGAGAAG 541 542 TITCAAGGGTCCTCACTGGTTGACCCCAAAATGTTCCCTTGACCA-ITGGCTGCGCT 600 CCCTGCCAGTCTCTTTAAAGAGATCTGTTCTGGGTGTTGACCACTCCAGAGAAG 653 Trcsagedercercacerederreacecaacacaterrecerreaceatrisecreceer 713 3 ATTCGGGAACGCGCCACAAGCAGCTGCTGAGCCATGAGGTGAAGGGGAAATCACCACC 114 AGTCTTGAAAGCGCCACAAGCAGCAGCTGCTGAGGCCATGGCTGAAGGGGAAATCACCACC Gaps 414 TACGGCTCACAGACACCAAATGAGGAATGTTTGTTTCTGGAAAGGCTGGAGGAGAACCAT 423 AATGGGAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTCTC /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall-KhoI (gtcgag); Oligo-dT primed using primer 'n, Query Match 87.7%; Score 559.8; DB 12; Length 821; Best Local Similarity 95.3%; Pred. No. 1.4e-153; Indels 601 A-ACCCCCAGAGCCTGAATTTGTAAGCAACTT 638 714 ATGCCCCAAGCCAGCAGAGCTGAATTTGTAAGCAACTT 752 http://image.llnl.gov
Plate: LLAM11764 row: k column: 23 0; Mismatches /tissue_type="hypothalamus" /organism="Homo sapiens" High quality sequence stop: 777. /clone lib="NIH MGC 96" clone="IMAGE:5302030" /db_xref="taxon:9606" Location/Qualifiers a NIH_MGC Library." /mol_type="mRNA" /lab host="DH10B Conservative 609; source Matches FEATURES ORIGIN ò g à 셤 ò 유 셤 à 셤 à à ద ò 셤 à g ò q ò g q à

MANSHOUT 7 MISSOUR A MISSOUR CADE BIRST HOW BORN LINEAR EST 21-ARP-199 BETAINTON WINGOL AN WILL CADE BIRST HOW ORDERED CORN CLOCK THAT SHOW THE WAS SERVED TO THE WILL OF SHALLS HERWING GROWTH EACTOR PRECEDEOR 1 SERVEDOR MISSOUR CLASS HIGH SHALLS HOUSE GROWTH EACTOR PRECEDEOR 1 MISSOUR MISSOUR CLASS HIGH SHALLS HOUSE GROWTH EACTOR PRECEDEOR 1 MISSOUR MISSOUR CLASS HIGH SHALLS HOUSE AND MISSOUR CLASS HIGH SHALLS HOW ON SADIEST HOUSE AND SHALLS HE WAS SHALLS HOW AND SHALLS HE WAS SHALLS HOW AND SHALLS HE WAS SHALLS HE WAS SHALLS HOW AND SHALLS HE WAS SHA	Db 234 TCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCATTACAAC 175 Qy 369 ACCTATATACCAAGAAGCATGCAGAGAAATTGGTTTGTTGGCTCAAGAAGAAGGAGGAGAAGAAGAAGAAGAAGAAGAAGAAG		Qy 489 CCAGTCTTCTGATTAAAGACTCTGTTCT-GGTGTTGACCACTCCAGAGAA 540	RESULT 8 BG706412 LOCUS BG706412 LOCUS BG706412 DEFINITION 602669744F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:4792378 5', ACCESSION BG706412 VERSION BG706412 VERSION BG706412 VERSION BG706412	EST. Homo sapiens Homo sapiens Homo sapiens Eukaryote; W Maumalia; Bu. I (bases 1 in Cases 2 in Cas	Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Thorye Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at: Plate: LiAM10670 row: h column: 11 High quality sequence stop: 710. PEATURES 1. 7144/Qualifiers 1. 7144/Qualifiers //db_Xref="RRMR" Ab. XRMR" //db_Xref="RRMR" Ab. XRMR" //db_Xref="RRMR" Ab. XRMR" //tissue trype="RRMR"	/lab_host="THIQB" //lone_lib="NHIQB" //lone_lib="NHIQB" //note="Corporality McCror: pBluescriptR (modified pBluescript KS+); Site_l: BamHI; Site_2: Sall-XhoI (Gregag); Oligo-dT primed using primer //THITITITITITITITITITITITITITITITY HONG To This is a primery library enriched for Hill-Length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MCC Library."	Query Match 78.6%; Score 501.6; DB 12; Length 714; Best Local Similarity 96.5%; Pred: No. 1.9e-136; Antiches 577; Conservative 0; Mismatches 14; Indels 7; Gaps 6; Oy 3 ATTCGGGAACGCCCACAAGCAGCTGCTGCTGCTGCTGGCTG
	A1590078 534 bp mRNA linear EST 21-APR-1 tm58c01.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2162304 similar to gb:M13361 HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1	Als90078 AL590078.1 GI:4599126 EST. Home sapiens (human)	Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 534)	NCL/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,	ares, Ph.D Ph.D. ity Genome stribution n/LLNL at:	1. :534 / Organism="Homo sapie" / mol type="maxkx" / db_xref="taxon:9606" / clone="lives:162304 / lab_host="hyde:1262304 / lab_host="hyde:12624 / lab_host="hyde:12624 / lab_host="hyde:12624 / lab_host="hyde:12624 / lab_host="hyde:12624 / lab_host="hyde:"hyde:12624 / lab_host="hyde:12624 / lab_ho	Length 534;	

λo	183 ACANGGA,CAGGAGGA,CCAGGACATTCAGCTGCAGCTCAGTGGGGAAAQCGTGGGGGAG 242	Best Loc Matches
qq	293 ACAAGGAACAGGACCACACATCAGCTGCAGCTCAGTGCGGAAAAGCGTGGGGAG 352	λō
., VQ	243 GIGIATAIAAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTA 302	qq
eg Q	353 GIGTATATAAAGAGTACCGAGACTGGCCAGTACTIGACCATGACACGACGACGGCTITTA 412	ò
δδ	303 TACGGCTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACGAT 362	DD
Db 4	413 TACGGCTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGCATAACAT 472	ò
	363 TACAACACCTATATATICCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGTGAGAAG 422	QQ
Db 4	473 TACAACACCTATATATCCAAGAAGATGCAGAGAAGAATTGGTTTGTTGGCCTCAAGAAG 532	λō
	423 AATGGGAACTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTCT- 481	qq
DQ S	533 AATGGGAGCTGCAAACGCGGTCCTCGGACTCACTATGGCCCAGAAAGCAATCTTGTTTTCTC 592	À
ζ.	482 CCCCTGCCAGTCTCTTCTGATTA-AAGAGTCTGTTCT-GGTGTTGACCACTCCAGAGA 539	qq
s qu	593 CCCCCTGCCAGTCTCTTCTGATTACAAGACTCTCTTCTGGGTGTTGACCACTCCAGAGA 652	λō
	540 AGITICGAGGGTCCTCACCTGGTTGACCCCAAAANGTICCCTIGACCATIGGCTGC 597	ηD
g G	653 AG-ITCGAGGGGTCCTCACCTGGTTGACCAAAATGTTCCCTTGACATTGGTGGGG 707	
RESULT 9		Db
AI077609/c LOCUS	AI077609 472 bp mRNA linear RST 24-cmp-1909	Ş,
DEFINITION	0y26d02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens_CDN_CLONE_HAGE:le66947 3' sina'smillar to gb.Ml3361 HEPARIN-BINDING GROWTH FACTOR PREFIRED 1 'unavan'	qa
ACCESSION	AIO77609 T. SALONASA I (NOMAN); MKNA Sequence. AIO77609 T. SALONASA	RESULT 10
KEYWORDS	A1077005:1 G1:541201/ EST.	AK035330 LOCHS
SOURCE	Homo sapiens (human) Homo sapiens	DEFINITION
	Eukaryota; Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi; Mammalia; Butheria; Primates; Catarxhini; Hominidae; Homo.	MOT 30 POOL
AUTHORS	1 (bases 1 to 472) NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	VERSION KEYWORDS
371.T	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	SOURCE
JOURNAL	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Engli cranhersmani aik cor.	ORGANISM
	This clone is available royalty-free through LLNL ; contact the	REFERENCE
	nformati	TILLE
	Insert Length: 649 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham	MEDLINE
FEATURES	High quality sequence stop: 1. Location/Qualifiers	PUBMED REFERENCE AUTHORS
Bonnos	1. 472 /organism="Homo sapiens"	TITLE
	/mol_type="mRNA" /db_xref="taxon:9606"	TANGLIOT
	/clone="IMAGE:1666947" /tissue_type="senescent_fibroblast"	MEDLINE
	/lab_host="DH10B (ampicillin resistant)" /clone lib="Soares senescent fibrohlasts where"	REFERENCE
	/note="Vector: pT7T3D (Pharmacia) with a modified polylinker V TYPE: phacemid: Site 1: Not T: Site 2. Enco	AUTHORS
	RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5]	
	TGTTACCAATCTGAAGTGGGGGCGGCATTTTTTTTTTTT	
	adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified purery vector	TITLE
	(Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento	JOURNAL
ORIGIN	Soares and M.Fatima Bonaldo."	PUBMED PUBMED REFERENCE

68.6%; Score 437.6; DB 9; Length 472;

Query Match

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AR035330 3404 bp mENA linear HTC 18-SEP-2003
Mus musculus adult male urinary bladder cDNA, RIKEN full-length
enriched library, clone:9530018E22 product:fibroblast growth factor
                                     128 CIGTAGCAACGGGGGCCACTICCTGAGGATCCTTCCGGATGGCACAGTGGATGGGACAAG 187
                                                                                                                                                        68 AGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTA 127
                                                                                                                                                                                                                                                 188 GGACAGGAGCGACCAGCACTTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGGAGGTGTA 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Oodeda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Wuramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKRN integrated Sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488 GCCAGTCTCTTCTGATTAAAGAGATCTGTTCT-GGTGTTGACCACTCCAGAG 538
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1; Gaps

14; Indels

96.8%; Pred. No. 1.1e-117;

0, Mismatches

457; Conservative

cal Similarity

QY 208 TTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGAGAGTATATAAAAGAGTACCGAGCTG 267 Db 358 TTCAGCTGCAGCTCAGTGCGGAAAGTGTATATAAAAGGTACGAAGCG 417 QY 268 GCCAGTGCAGCGCACAGCGGCTTTTATACGGCTCACAAACAGG 417 Db 418 GCCAGTACTTGGCATGGACACCGAGGGCTTTTATACGGCTCACAAACAGG 477 QY 328 AATGTTGGCATGGACACCGAAGGCTTTTATACGGCTCACAAACAA		RESULT 11 B1692283 LOCUS B1692283 B1692283 B1692283 B1632281 ACCESSION B1632283 WERNARDS B1622283 WERSION B1622283 WEST B16554912 SOURCE Was musculus (house mouse) ORGANISM Mus musculus (house mouse) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom; Mus musculus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom; Mus masculus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom; Mus musculus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butlenaia; Butleria; Rodentia; Sciurognathi; Muridae; Mus: Musmalia; Butleria; Rodentia; Sciurognathi; Muridae; Mus: AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) COMMENT Contact: Robert Strausberg, Ph.D. Contact: Robert Strausberg, Ph.D. COMMENT Contact: Robert Strausberg, Ph.D. CONA Library Preparation: Life Technologies, Inc. CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Inc.Consortium (LINL) DNA Library Drocure Consortium (LINL) Repart Library Drocure Consortium (LINL) Library Drocure Consortium (L	/organism="Mus musculus" /mol_type="maxNa" /mol_type="maxNa" /strain="PRJN-3" /db_xref="taxon:10090" /clone="MaxBs:5370612" /lassue_type="tumor, biopsy sample" /dev_stage="5 months" /lab.ost="Mill Toole "Mill Toole" /lab.ost="NoI CGAP Mam2" /lone lib="NOI CGAP Mam2" /lone lib="NOI CGAP Mam2" /lone lib="NOI CGAP Mam2" /lone lib="NOI CGAP Mam2" /lone lib-tst="Mill Toole"
TITLE Punctional annotation of a full-length mouse cDNA collection JOURNAL Nature 409, 685-690 (2001) REFERENCE Group Phase I & II Team. TITLE Group Phase I & II Team. TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs JOURNAL Nature 420, 563-573 (2002) REFERENCE 6 (bases I to 3404) AUTHORS Adachi,J. Aizawa,K. Akimura,T., Arakawa,T., Bono,H., Carninci,P., Hayashida,K. Hayatsu,N., Hinamoto,K., Hiraoka,T., Hirozane,T., Hori,P., Imotani,K., Ishi,Y., Itch,M., Kagawa,T., Kasukawa,T., Katch,H., Kawai,J., Kojima,Y., Koho,S., Komno,H., Konda,M., Katch,H., Kawai,J., Kojima,Y., Koho,S., Komno,H., Konda,M., Nakamura,M., Nishi,K., Nomira,Y., Nishi,K., Sakazume,N., Nakamura,M., Nishi,K., Nomira,K., Shinagawa,A., Shinaki,Y., Tagami,M., Tagawa,A., Shinagawa,A., Shiraki,T., Sakazume,N., Sabo,P., Y., Tagami,M., Tagawa,A., Shiraki,F., Takaku,Hahira,S., Takada,Y., Tanaka,T., Tomari,A., Toya, T., Yasunishi,R., Takaku, Akahira,S., Takada,Y., Tanaka,T., Tomari,A., Toya,T., Yasunishi,A., Toya,T., Yasunishi,A., Toya,A., Y., Tagawa,A., Tayaha,A., Yasunishi,A., Tayahira,A., Toya,T., Yasunishi,A., Tayahira,A., Yasunishi,A., Tayahira,A., Yasunishi,A., Tayahira,A., Toya,T., Yasunishi,A., Tayahira,A., Tomari,A., Towari,A., Toya,T., Yasunishi,A., Tayahira,A., Towari,A., Towari,A., Toya,T., Yasunishi,A., Toya,T., Yasunishi,A., Tayahira,A., Toya,T., Yasunishi,A.,	Muramatsu, M. and Hayashizaki, Y. TITLE Direct Submission JOURNAL Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research (Croup, RIKEN) Cenomic Sciences Center (SSC), RIKEN Yokohama Institute, 1-7.22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegge.riken.go.jp, URLihttp://genome.gsc.riken.go.jp/, Tel:81-45-503-922, FAX:81-45-503-9216) COMMENT CDNA library was prepared and sequenced in Mouse Genome Bncyclopedia broject of Genome Exploration Research droup in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Anhal Research in Riken contributed to		Query Match 68.1%; Score 434.6; DB 11; Length 3404; Best Local Similarity 84.3%; Pred. No. 2.5e-116; Anders 512; Conservative 0; Mismatches 69; Indels 26; Gaps 1; QY 28 GCRGCRAGCCRAGGCRARCCRCCCCCCCCCCCCCCCCCC

13; Conservative 0; Mismatches 66; Indels 28; Gaps 2;	GCTSCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGGCCTGACCGACC		ACCTGCCTCTAGGAAACTAGAAAAGCCCAAACTGCTGCTACTGCAGCAGCGGGGGCCACT	9 TCCTGARGARICCTICCGGARGGCACAGTGGGATGGGACAGGACGACCAGCACCA 207 	TICAGCIGCAGCICAGIGCGGAAAGCGIGGGGGGTGTATATAAAGGTACCAGACIG 267 	GCCAGTACTTGGCCATGGACACCGACGGCTTTTATACGGCTCACAGACACCAAATGAGG 32	GCCAGTACTTGGCCGTGGACACCGAAGGGCTTTTATACGGCTCGCAGCACACCAATTGAG AATGTTTGTTGCTGGAAAGGCTTGGAAAGGGCTTTTTATACAAGAGGCTGCGAGCACAGAAGAGGAGAGGAGAGAGA	ANTOTICOTICOTASABAGGCIVGAKGARAACCATTACAACACCTATATATCCAAGAAGC 387 	AIGCAGAGAAAATIGGITIGITGGCCICAAGAATGGGGGCTGCAAACGGGGTCCTA 447 	AAACICACIATIGGCCAGAAAGCAATCITIGTITCTCCCCCCGGGTCTCTTCTGATTAAA	SASTITUTE TO STREAM CANTON AGAINT TO AGAGGICT CACTON TO THE SET OF THE STREAM SET OF	CCCAAAAATGTTCCCTTGACCATTGGCTGCGCTAACCCCCCAGCCCACAGAGCCTGAATTTT	CCTACCATGITCCCTTGACCATTGGCTGCGCTAACCTCAGGCCACAGAGCCTGAATTT		GTAACA 756	BF956865 RCI-NNO233-221100-011-h12 NNO233 Homo sapiens CDNA, mRNA sequence. BF956865.1 BF956865.1 BF956865.1 BF956865.1 BF956865.1 GI:12374140 BEST BFOOM Sapiens Homo sapiens	
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Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-NN0233-2100-011-12&t2=2000-11-22&t4=1)
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High quality sequence start: 11
High quality sequence stop: 461.
                                                                                                                                                                                                                                                                /dev_stage="Addil"
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Site 2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
Profiles into the pUC 18 vector. Reverse transcription of
tissue mRNR and cDNA amplification were performed under
low stringency conditions.
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Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Altasner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Butchew,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.B., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 GCCCAAACTCCTCTACTGTAGCAACGGGGCCACTTCCTGAG-GATCCTTCCGGATGGCA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 CAGTGGATGGGACAAGGGACGAGGGACCAGCACTTCAGCTGCAGGTCAGTGCGGAAA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CAGTGGATGGGACAAGGGACGACGACACATTCAGCTGCAGCTCAGTGCGGAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 GCGTGGGGGAGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 AGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGAAGAATTGGTTG 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 AGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGAATTGGTTTGTTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 GCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCTCGGGCTCACTATGGCCAGAAAGCAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear HTC 19-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | GGCCAAACACCTCTACTGTAGCAACGGGGCCACTTCCTGAGAGATCCTTCCGGATGGCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472 TCTTGTTTCTCCCCCCTGCCAGTCTCTTCTGATTAAAGAGATCTGTTCT-GGTGTTGACCA 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus fibroblast growth factor 1, mRNA (cDNA clone IMAGE:5370612), containing frame-shift errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 66.5%; Score 424.2; DB 10; Length 461; Best Local Similarity 97.8%; Pred. No. 1e-113; Matches 451; Conservative 0; Mismatches 8: Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            531 CTCCAGAGAAGTTTCGAGGGTCCTCACCTGGTTGACCCCA 571
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                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                    /mol_type="mRNA"
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                                                                                                                                              Location/Qualifiers
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		Carninci, P., Pranqe, C., Raha. S.S., Lorniellano N. a. Daravo C.		
		Abramson, R.D., Millahy, S.D., Logask, S.A., McDwan, P.D., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hully, K.S.M., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,	gg Å	406 GCCAGTACTTGGCCATGACACCGAAGGGCT328 AATGTTTGTTCCTGGAAGGCTGGAGGGAGAGAGAGAGAGA
		Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevohenko, Y., Bouffaxed, G.G., Blakesley, R. W., Touchman, J.W., Green, E.D.	අ දි	466 AAIGICICICICCIGGAAAGGCTGGAAGAAAG
		<pre>DicKson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.B., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M. A.</pre>		526 ATGCGGAGAAGAATIGGTTIGTIGGCCTCAA
	TITLE JOURNAL MEDLINE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 22388257	oy da	448 AAACTCACTATGGCCAGAAAGGAATCTTGTTT 586 GGACTCACTATGGCCAGAAAGCCATCTTGTTT
	PUBMED REFERENCE AUTHORS	12477912 2 (bases 1 to 2206) Strausberg,R.	λ d	508 GAGATCTGTTCTGGTTGACCACTCCAGAGA 646 GGAGTCCTTCTT
	TITLE JOURNAL	Direct Submission Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		568 CCCAAAATGTTCCCTTGACCATTGGCTGCGC
	REMARK COMMENT	usa NIH-MGC Project URL: http://mgc.nci.nih.gov Ontaat: MGC help desk	ζ	628 GTAAGCA 634
		Email: cgapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D.	da	 740 GTAAGCA 746
		LONA intrary Preparation: Life Technologies, Inc. CONA Library Arrayed by: The TA.A.G.E. Consortium (LLAL) DNA Sequencing by: Baylor College of Medicine Human Genome	RESULT 14	
		Sequencing Center Center code, BCM-HGSC	LOCUS	AI119291 ue95c07.yl Sugano mouse embryo mew
				IMAGE:1498860 5' similar to gb:Ml3 PRECURSOR 1 (HUMAN); mRNA sequent
		ounstance, V.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.	ACCESSION VERSION KEYWORDS	AI119291 AI119291.1 GI:3519615 FST
		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LAM, at: http://image ll.nl.cov	SOURCE	Mus musculus (house mouse) Mus musculus
		Series: IRAX Plate: 53 Row: n Column: 3 This clone was selected for full langth semisoring harmon;	,	Eukaryoca; Metazoa; Chordata; Cran. Mammalia; Eutheria; Rodentia; Sciu:
		passed the following selection criteria: matched mRNA gi: 6753849 This clone has the following model of the following model.	REFERENCE AUTHORS	<pre>1 (bases 1 to 663) Marra,M., Hillier,L., Allen,M., Bo</pre>
	FEATURES SOUICE			Geisel, S., Kucaba, T., Lacy, M., Le, I Schellenberg, K., Steptoe, M., Tan, F
		/organism="Mus musculus" /mol_type="mRNA"	ያ. የ.	Inelsing, B., Wylle, T., Lennon, G., & Waterston, R. The Washi Will Manne and American
		/strain="FVB/N-3" /db_xref="taxon:10090"	JOURNAL	Inc Masuu-Anmi Mouse EST Froject Unpublished (1996) Contact: Marra M/Mouse Est Droject
		/clone="IMAGE:5370612" /tissue_type="Mammary tumor. MMTV-LTR/INT3 model. 5 month		WashU-HMM Mouse EST Project
				Mashington University School of Med 4444 Forest Park Parkway, Box 8501, Tel: 214 266 1866
	ORIGIN	/lab_host="WH10B" /note="Vector: pCMV-SPORT6"		Fax: 314 286 1810 Email: mouseest@watson.wustl.edu
	Query Match			This clone is available royalty-fre IMAGE Consortium (info@image.llnl.g
	Best Local Simi Matches 510;	larity 84.0%; Pred. No. 2.7. Conservative 0; Mismatches		Seq primer: custom primer used High quality sequence stop: 527
	0y 2	28 GCTGCTGAGCCATGGCTGAAGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTA 87	FEATURES	Location/Qualifiers 1663
	Db 16	168 GCTGCCGAGGCAAGGGGGGGGGTCACATTCGCAGCCCTGACCGAGAGGTTCA 227		/organism="Mus musculus" /mol_type="mRNA"
	8 . 8	88 ATCTCCCCCAGGGATTACAAGAAGCCCAAACTCCTCTACTCGTAGCAACGGGGCCACT 147		/strain="C57BL" /db_xref="taxon:10090" /rlone="IMAGE:1400000"
		28 ACCIGACITIAGGAAACTACAAAAAGCCCAAACTGCTCTACTGCAGCAAGGGGGGCCACT 287		/dev_stage="embryo, 14 dpc /lab host="muling"
_		148 ICCIDAGARICCTICCGGATGCCAAGGTGATGGGACAGGGACAGGACAG		/clone_lib="Sugano mouse e /note="Vector: pME18S-FL3;
_	Qy 20	208 TTCAGCTCCAGCTCAGTCCGAAAGCGTTGAAAAGCGTTGTATATAATAATAAAAAAGCTTGTAATAATAATAAAAAAAA		Site_2: DraIII (CACCATGTG) with an oligo(dT) primer
-				double-stranded cDNA was 1 [IGITGGCCTACTGG], digested
5	26ί	268 GCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTCACAGACACCCAAATGAGG 327		Sites of the pME18S-FL3 ve CACCATGIG). Xhol should be insert. Size selection was
				51 101200110 2111

-	328 ANTGITICTICCIOGAAAGGCIGGAGGAGAACCATIACAACACCIAINIAITATCCAAGAAGC 387
_,	388 ATGCAGAGAAAATTGGTTTGTTGGCCTCAAGAAGAATGGGAGCTGCAACGCGGTCCTA 447
,	448 AAACICACIATIGGCCAGAAAGGAATCITGITICTCCCCCTGCCAGTCTCTTCTGATTAAA 507 586 GAACICACIATIGGCCAGAAAGCATCTTGITITCTGCCCCTCCCGGTGTCTTCTGACTAGA 645
•	508 GAGATCTGTTCTGGTGTTGACCACTCCAGAGAAGTTTCGAGGGGGCTCTGGTTGAC 567
u	62
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, NO	AI119291 663 bp mRNA linear EST 02-SEP-1998 ue95c07-yl Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE:149886 5' similar fo ch.Mllst HERNDRY Erhnyng chomum
z	sequence.
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Σ	Mus musculus Mus musculus Mawmalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mawmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
ചഗ	ouque,
	Getset,S., Aucada,T., Lady,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
J	The WashU-HHMI Mouse EST Project Oppublished (1996)
	licinep
	"
	through LLNL ; contact
	v) for further
	High quality sequence stop: 527.
g G	
	/mol_type="mRNA" /strain="CS7BL"
	/db_xref="taxon:10090" /clone="1MAGE:1498860"
	/dev_stage="embryo, 14 dpc" Jab host="PH108" Jab host="PH108"
	/cloude_lib="Sugano mouse empiryo newa" /note="Vector: pME18S-Fil3; Site_l: Drail! (CACTGTOTG); Site_l: Drail! (CACCATGTS) - 1st errand chun cac national
	with an oligo(dr) primer (ATGTGGCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
	[19r1043CTACTAG], digested and cloned into distinct DraIII sites of the pMEIBS-Fill vector (5' site CACTGTGTG, 3' site CACTGTGTG, 4' site
	CACCAIGIG). Anoi snould be used to isolate the cDNA insert. Size selection was performed to exclude fragments

DEFINITION RESULT 15 BI331990 ORGANISM TITLE JOURNAL COMMENT ACCESSION REFERENCE AUTHORS KEYWORDS VERSION SOURCE à g à qq a g à g a ò à 셤 g q à ò ò ð

1. .855
/organism="Mus musculus"

/mol_type="mRNA"

Location/Qualifiers

source

FEATURES

Job time : 2851 secs ORIGIN 엄 ò g g δ 엄 ò g à д à à g à ò 0; 88 ATCTGCCTCCAGGGAATTACAAGAGCCCAAACTCCTCTACTGTAGCAACGGGGCCACT 147 EST 30-JUL-2001 TCCTGAGGATCCTTCCGGATGGCACAGTGGATGGGACAAGGGACAGGAGCGACCAGCACA 207 TTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGGGGTGTATAAAAGAGTACCGAGACTG 267 268 GCCAGTACTTGGCCATGGACACCGACGGCTTTTATACGGCTCACAGACACCAAATGAGG 327 388 ATCCAGAGAAGAATTGGTTGTTGGCCTCAAGAAGAATGGGGAGCTGCAAACGCGGTCCTA 447 28 GCTGCTGAGCCAIGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCAGAAGTTTA 87 285 TCTTGAGGATCCTTCCTGATGGCACCGTGGATGGGACAAGGGACAGGGACGACGACA 344 TTCAGCTGCAGCTCAGTGCGGAAAGTGCGGGCGAAGTGTATATAAAGGGTACGGAGACCG 404 328 AATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATTCCAAGAAGC 387 465 AATGICIGCICCIGGAAAGGCIGGAAGAAACCAITIAIAACACTIACACCICCAAGAAGC 524 448 AAACTCACTATGGCCAGAAAGCAATCTTGTTTCTCCCCTGCCAGTCTCTTCTGATTAAA 507 585 GGACTCACTATGGCCAGAAAGCCATCTTGTTTCTGCCCCTCCCGGTGTCTTCTGACAGAAA Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 855 bp mRNA linear EST 30-JUL-201 602984193Fl NOI_CGAP_Li9 Mus musculus CDNA clone IMAGE:5137246 5', mRNA sequence. 0; Gaps DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can be National Institutes of Health, Mammalian Gene Collection (MGC) <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTRCTGCTCTARARGCTGG and 3' end primer GGACCTGCAGCTGAGCACA." CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML) Score 408.2; DB 9; Length 663; Pred. No. 6.4e-109; 0; Mismatches 53; Indels 0 found through the I.M.A.G.E. Consortium/LLNL at: Email: cgapbs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. http://image.llnl.gov Plate: LLAM11337 row: i column: 23 Contact: Robert Strausberg, Ph.D. NIH-MGC http://mgc.nci.nih.gov/. High quality sequence stop: 752. Mus musculus (house mouse) BI331990.1 GI:15016647 64.0%; 89.2%; 508 GAGATCTGTTCTG 520 645 GGAGTCTGTTCTG 657 Matches 440; Conservative (bases 1 to 855) Unpublished (1999) Best Local Similarity Mus musculus BI331990 EST. 148 208 345 Query Match ORIGIN

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88 ATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 ACCTGCCTCTAGGAAACTACAAAAAGCCCAAACTGCTCTACTGCAGCAACGGGGGCCACT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 TCTTGAGGATCCTTCCTGATGGCACCGTGGATGGGACAAGGGACAGGACACAGCACA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 TICAGCIGCAGCICAGIGCGGAAAGIGCGGAGGGGAAGIGTATAIAAAGGGTACGGAGACCG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484 AATGICIGITCCIGGAAAGGCIGGAAGAAACCAITATAACACITACACTCCAAGAAGC 543
                                                                                                                     /note="Organ: liver, Vector: pCNV-SPORT6; Site_1: Not1, Site_1: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 TCCTGAGGATCCTTCCGGATGGCACAGTGGATGGGACAGGGACAGGAGCGACCAGCACA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 ITCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGGAGGTGTATAAAAGAGTACCGAGACTG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 GCCAGTACTTGGCCATGGACACCGACGGCTTTTATACGGCTCACAGACACCAAATGAGG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 AATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 AIGCAGAGAAAIIIGIIIGIIIGICCICAAGAAGAAIGGGAGCIGCAAACGCGGICCIA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            544 ATGCGGAGAAGAACTGGTTTGTGGGCCTCAAGAAGAACGGGAGCTGTAAGCGCGGTCCTC 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448 AAACTCACTATGGCCAGAAAGCAATCTTGTTTCTCCCCTGCCAGTCTCTTCTGATTAAA 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      604 GGACTCACTATGGCCAGAAAGCCATCTTGTTTCTGCCCCTCCCGGTGTCTTCTGACTAGA 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 GCTGCTGAGCCATGGCTGAAGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTA 87
                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                               63.3%; Score 404; DB 12; Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                   50; Indels
                                                            /lab_host="DH10B (Tl phage-resistant)"
/clone_lib="NCI_CGAP_Li9"
                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.3e-107;
                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
/db xref="taxon:10090"
                        /clone="IMAGE:5137246"
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                                                                                                                                                                                                                                                                                                                                                        89.7%;
                                                                                                                                                                                                                                                                                                                                                                                               434; Conservative
                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 434; Conserval
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                                                                                                                                                                                                                                                                                                                            Query Match
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strain="FVB/N"

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

Match Length DB

Score

using sw model nucleic - nucleic search, ĕ

August 24, 2004, 20:02:52; Search time 4175 Seconds Run on:

(without alignments) 6623.438 Million cell updates/sec

US-10-022-554A-3 Title: Perfect score:

1 gaattcgggaacgcgccaca......cctgaatttgtaagcaactt 638 Sequence:

OLIGO NUC Scoring table:

Gapop 60.0 , Gapext 60.0

3470272 seqs, 21671516995 residues

Searched:

0 Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

gb_ba:* Database :

gb_htg: *
gb_om: *
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gb_pl: *

gb_ro:*
gb_sts:*
gb_sy:*
gb_un:*
gb_vi:*
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em_om:*
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em_htg_other:* em_htg_mus:* em htg pln:*
em htg rod:*
em htg mam:*

em_htgo_hum:* em_htgo_mus:* em_htg_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_htgo_other:*

SUMMARIES

Query

Result

A49428 Sequence 13 109499 Sequence 13 109297 Sequence 13 109297 Sequence 10 E25526 Sugar chain E25510 Sugar chain E25522 Sugar chain E25522 Sugar chain E25523 Sugar chain E25523 Sugar chain E25525 Sugar chain E25515 Sugar chain E25525 Sugar chain E25525 Sugar chain E25525 Sugar chain E25515 Sugar chain E25615 Sugar chain E25515 Sugar chain E38007 Process for E38007 Proces 102042 Sequence 5 108496 Sequence 7 M13361 Human beta-108090 Sequence 4 M23017 Human hepar ACO05370 Homo sapi ACO91022 Homo sapi ACO10489 Homo sapi ACO16560 Homo sapi ACO0659 Arrificial ACO070 Arrificial X65778 H.sapiens a S67291 Homo sapien BC032697 Homo sapi X51943 Human mRNA AR428605 Sequence AX481449 Sequence AR380845 Sequence Sequence 3 Description 102042 108496 HUMECGFB 108090 109138 BC032697 HSHPGF1 AR380845 HSAFGF S67291 AR428605 AX481449 E38002 AX908985 E38004 HUMFGFAB AC091822 AC010489 AC016560 BD044518 AC005370 HUMFGFAL HUMHBGF1 108499 109297 1039287 1039287 1039287 103928 A49428 E38007 32.3 363 31.8 363 31.8 563 31.7 249 30.6 503 30.6 1082 30.6 76416 30.6 14643 30.6 19734 29.2 454 40.0 39.8 39.7 37.8 40.4

RESULT 1

linear PAT 21-MAY-1993 1 (bases 1 to 638)
Jaye,M., Burgess,W., Maciag,T. and Drohan,W.
Recombinant DNA vector encoding human endothelial cell growth Patent: US 4868113-A 5 19-SEP-1989, Rorer Biotechnology, Inc.; King of Prussia, Location/Qualifiers 638 bp ss-DNA /organism="unknown" /mol_type="unassigned DNA" 102042 638 bp ss Sequence 5 from Patent US 4868113. I02042.1 GI:270417 1. .638 Unclassified. Unknown. Unknown source DEFINITION ORGANISM ACCESSION AUTHORS TITLE REFERENCE VERSION KEYWORDS JOURNAL FEATURES SOURCE

ORIGIN

Query Match 76.0%; Score 485; DB 6; Length 638; Best Local Similarity 99.5%; Pred. No. 1.2e-250; Matches 635; Conservative 0; Mismatches 3; Indels

0; Gaps

3; Indels

	0;
	Gaps
	0;
	Indels
250;	3,
Pred. No. 1.2e-250,	Mismatches
Pred.	0; Mi
99.5%;	ative
nilarity	Conservative
ıl Sir	635;
Best Local Similarity	Matches

Matches	635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	J
δ	1 GAATTCGGGAACGCGCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCA 60	I
QQ	1 GAAITCGGGAACGCGCCACAAGCAGCTGCTGAGCCCATGCCTSAAGGGGAAATCACCA 60	O.
δλ	61 CCTICACAGCCCTGACCGACAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAC 120	Д
đ	61 CCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAC 120	O.
λο 1	121 TCCTCDACTGTBGCAACGGGGCCACTTCCTGAGGATGCTTCCGGATGCACGTGGATG 180	Ω
ΩP	121 TCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATCCTTCCGGGATGGCACAGTGGATG 180	o
Ğ	181 GGACAAGGGACGACCAGCACACATTCAGCTGCAGGTGCGGGAAAGCGTGGGGG 240	Ω
qq	181 GGACAAGGACAGGACCAGCACACACACTCCAGCTCCAGTGCGGAAAGCCTGGGGGG 240	ø
ò	241 AGGIGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACGGAGCTTT 300	A
Ор	241 AGGIGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTT 300	a
ζ	301 TATACGCTICACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACC 360	Ā
qq	301 TATACGCTCACAGACACCAAATGAGGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACC 360	i
۲۵	361 ATPACAACACCIATATATCCAAGAAGCATGCAGAGAAGATTGGTTTGTTGGTGGCCTCAAGA 420	± i i
qq	361 ATTACAACACCTATATATCCAAGAAGCATGCAGAGAATTGGTTTGTTGGCCTCAAGA 420	ומה
λŏ	421 AGAATGGGAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTC 480	A Þ
qq	421 AGAATGGGAGCTGCAAACGCGGTCCTCGGACTCACTATGGCCAGAAAGCAATCTTGTTTC 480	⊠ ⊠
λõ	481 TCCCCTGCCAGTCTCTTCTGATTAAAGAGATCTGTTCTGGTGTTGACCACTCCAGAGAA 540	
οqα	481 TCCCCTGCCAGICTCTTCTGATTAAAGAGATCTGTTCTGGTGTTGACCACTCCAGAGAA 540	22
λŌ	541 GITICGAGGGGCCCTCACCTGGITGACCCCAAAAATGITCCCTTGACCAITGGCTGCGT 600	E
qq	541 GTTICGAGGGCTCCTCACCTGGTTGACCCCAAAAATGTTCCCTTGACCATTGGCTGCGCT 600	
λō	601 AACCCCCAGCCCAGAGCCTGAATTTGTAAGCAACTT 638	ō
qq	601 AACCCCAGCCCAACACACCTGAATTTGTAAGCAACTT 638	
RESULT 4		ć
LOCUS	638 bp	3
ACCESSION	TION PACENCES	ä
KEYWORDS	61686:15	ð
SOURCE	Unknown. Unknown.	ď
REFERENCE	Unclassified. 1 (bases 1 to 638)	õ
AUTHORS	Fiddes, J.C., Abraham, J.A. and Protter, A. Recombinant fibroblast growth factors	ä
JOURNAL FEATURES		õ
source	1 /org	ద
ORIGIN	/mol_type="unassigned DNA"	ð
Query Match	68.0%; Score 434;	셤
Best Loca Matches	<pre>similarity 100.0%; Pred. No. 4.8e-223; 1; Conservative 0; Mismatches 0; Indel</pre>	ò
ò	13 GCGCCACAAGCAGCAGCTGGTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCC 72	අය
Db	65 GCGCCACAAGCAGCAGCTGAGCCATGAGCGGAAATCACCACCTCACAGCCC 124	ò
δy	73 TGACCGAGAAGTITTAATCTGCCTCCAGGGAAITACAAGAAGCCCCAAAACTCCTCTACTGTA 132	d d
Db 1		δ

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/note="FGE; Region: Fibroblast growth factor. Fibroblast growth factors are a family of proteins involved in growth and differentiation in a wide range of contexts. These
                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MAEGEITTFTALTEKFNLPPGNYKKPKLLYCSNGGHFLRILPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                             TVDGTRDRSDQHIQLQLSAESVGEVYIKSTETGQYLAMDTDGLLYGSQTPNEECLFLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth factors cause dimerisation of their tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptors leading to intracellular signaling. There are currently four known tyrosine kinase receptors for fibroblast growth factors. These receptors can each bind several different members of this family. Members of this family have a beta trefoil structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 GCGCCACAAGCAGCAGCTGAGCCATGAGGGGAAAATCACCACCTTCACAGCCC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 TGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCCAAACTCCTCTACTGTA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 GCAACGGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGGACAAGGGACA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 GGAGCGACCACCACTTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGAGCTGTATATAA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 GGAGCGACCAGCACTTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGGGTGTTTTTTA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 AGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTCAC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 AGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCATTACAACACT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 ATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGCCTCAAGAAGAATGGGAGCT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear PRI 12-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 GCGCCACAAGCAGCAGCTGCTGAGGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 AGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGCTTTTTATACGGCTCAC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 AGACACCAAATGAGGAATGTTTGTTCCTGGAAGGCTGGAGGAGAACCATTACAACACT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="synonyms: FGFA, AFGF, ECGF, ECGFA, ECGFB, HBGF1,
ECGF-beta, FGF-alpha, GLIO703"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLEENHYNTYISKKHAEKNWFVGLKKNGSCKRGPRTHYGQKAILFLPLPVSSD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fibroblast growth factor; growth factor; heparin-binding growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 GCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGGGACAAGGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.0%; Score 434; DB 9; Length 1073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 4.6e-223;
                            note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. w...
                                                                                                                                                                                                                                                                                              /product="FGF1 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="CDD:pfam00167"
                                                                                                                                                                           db_xref="LocusID:2246"
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                                                                                                                                                                                                                                                                 /codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433 GCAAACGCGGTCCT 446
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Best Local Similarity
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Klausner, R.D., Collins, F.S., Magner, L., Shenmen, C.M., Schuler, G.D.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Alschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Staplechon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Millahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hullyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Scheubers, S.,

Sanchez, A., Whithing, M., Madan, A., Young, A.C., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, W.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
                                                                                                                               BEC032697 BEC032697 Inhear PRI 06-0CT-2003 Homo sapiens fibroblast growth factor 1 (acidic), mRNA (cDNA clone MGC:44667 IMAGE:5403677), complete cds.
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Mikler, N. Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.C., Brenk, R. Brndkey, C., Brocks, S.,

Dietrich, N.L., Grante, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Maduro, C.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J. C.,

McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 69 Row: d Column: This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15055546.
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarthini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (06-JUN-2002) National Institutes of Health, Mammalian
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Young, A., Zhang, L.-H. and Green, E.D.
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Web site: http://www.nisc.nih.gov/
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Tissue Procurement: ATCC
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DEFINITION Sequence 1390 from patent US 6607879. ACCESSION AR380845 ACCESSION AR380845.1 G1:40088479 KEYNORDS SOURCE Unclassified. Vowpositions for the detection of blood cell and immunological response gene expression Unuclassified. Voypanism="unknown" V-490 V-49	Ouery Match Query Match Best Local Similarity 10:0%; Pred. No. 2.2e-214; Matches 418; Conservative 0. Mismatches 0; Indels 0; Gaps 0; QY 29 CTGCTGAGCCATGAGGGGAAATCACCACCTTCACACCCTGACCAGAGATTAA 88		HSAFGF ACCESSION K65778 K65778 K65778 HOMO sapiens GEANISM HOMO sapiens DEVERTORS HOMO sapiens CREANISM HOMO sapiens TUTLE AN acidic fibroblast growth factor protein generated by alternate JOURNAL JSEP. Med. 175 (4), 1073-1080 (1992) MEDLINE PUBMED SOURCE O'CHANISM HOMO Sapiens HOMO O'CHANISM HOMO O'CHA
REFERENCE 1 (bases 1 to 2259) AUTHORS 2 (bases 1 to 2259) AUTHORS 3 (but I.M. TITLE Davis Medical Research Centre, The Ohio State University, 480 West Constion/Qualifiers 1 (coation/Qualifiers 1 (coation/Qualifiers) AUTHORS 3 (cource //roganism="Homo sapiens" //mol_type="mRNA"	/db_xref="taxon:9606" /clone="pHeGF1.1, 1.2, 1.3, 1.4 and 1.5" /tlssue_type="brain stem" /dev_stage="neonate" /dev_stage="neonate" /dev_stage="neonate" /dev_stage="neonate" /dev_stage="neonate" /dev_stage="neonate" /forden start=1 /protein_id="caa36206.1" /db_xref="caa36206.1" /db_xref	Query Match 68.0%; Score 434; DB 9; Length 2259; Best Local Similarity 100.0%; Pred. No. 4.3e-223; Aldels 0; Gaps 0; Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 13 GGGCACAAGGAGAGAGAGAGAGAGAGAAATCACACACTTCACAGCC 72	133 GCAACGGGGCCACTTCCTCGAGGTCGATCGCACGGTGGATGGCACAGGGCAC 192

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ORIGIN

Zhao, X.M., Yeoh, T.K., Hiebert, M., Frist, W.H. and Miller, G.G.
The expression of acidic fibroblast growth factor (heparin-binding growth factor-1) and cytokine genes in human cardiac allografts and S67291
464 bp mRNA linear PRI 06-MAR-2001
Homo sapiens acidic fibroblast growth factor (aFGF) mRNA, partial 89 TCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTT 148 61 TCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTT 120 149 CCTGAGGATCCTTCCGGATGGCACAGTGGGACAAGGGACAGGACAGGACCAGCACCAT 208 121 CCTGAGGATCCTTCCGGATGGCACAGTGGGATGGGACAAGGGACAGGACCAGCACT 180 209 TCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGGAGGTGTATATAAAGAGTACCCGAGACTGG 268 181 TCAGCTGCAGTGCGGAAAAGCGTGGGGGGGGGGGTGTATAAAAGAGTACCGAGACTGG 240 269 CCAGTACTIGGCCAIGGACACCGACGGCTTITATACGGCTCACAGACACCAAATGAGGA 328 329 AIGITIGITCCIGGAAAGGCIGGAGGAGAACCAITACAACACCIATATATCCAAGAAGCA 388 301 ATGITICITCCIGGAAAGGCIGGAGAAACCATIACAACACCIAIAIAITCCAAGAAGCA 360 29 CIGCIGAGCCAIGGCIGAAGGGGGAAAICACCACCIITCACAGCCCIGACCGAGAAGIIIAA 88 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 389 IGCAGAGAAATIGGITIGIIGGCCTCAAGAAGAAIGGGAGCIGCAAACGCGGICCI 446 Gaps GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 140709] from the original journal article. This sequence comes from Fig. 2A. ö 65.5%; Score 418; DB 9; Length 490; 100.0%; Pred. No. 2.2e-214; 0; Indels linear tissue_type="cardiac allograft" Transplantation 56 (5), 1177-1182 (1993) 94069734 0; Mismatches /organism="Homo sapiens" 464 bp /mol_type="mRNA" /db_xref="taxon:9606" Location/Qualifiers /gene="aFGF" /gene="aFGF" Homo sapiens (human) GI:456823 (bases 1 to 464) 418; Conservative 1. .>464 .464 .>464 Local Similarity Homo sapiens S67291.1 T cells 7504343 S67291 S67291 Query Match DEFINITION source Matches ORGANISM RESULT 10 ACCESSION REFERENCE gene JOURNAL MEDLINE PUBMED KEYWORDS CDS REMARK FEATURES TITE VERSION SOURCE ф g ò ð a à à g ò g ò 셤 ò g

/note="This sequence comes from Fig. 2A; heparin-binding growth factor-1"

/product="acidic fibroblast growth factor"

codon_start=1

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ORIGIN

99 GGGAATTACAAGAAGCCCAAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 158 PAT 18-DEC-2003 61 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAAGGGGGCCCACTTCCTGAGGATC 120 159 CTTCCGGATGGCACAGTGGATGGGACAGGACAGGAGCGACCAGCACATTCAGCTGCAG 218 219 CTCAGTGCGGAAAGCGTGCGGGGGGTGTATAAAGAGTACCGAGACTGGCCAGTACTTG 278 181 CTCAGTGCGGAAAGCGTGGGGGGGGTGTATAAAGAGTACCGAGACTGGCCAGTACTTG 240 241 GCCATGGACACCGACGGGCTITTATACGGCTCACAGACACCAAATGAGGAATGTITGTTC 300 339 CIGGAAAGGCIGGAGAGAACCAITACAACACCIATATATCCAAGAAGCAIGCAGGAGA 398 301 CTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGAAG 360 1 AIGGCIGAAGGGGAAAICACCACCTICACAGCCCTGACCGAGAAGITIAAICIGCCICCA 60 99 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 158 61 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 120 159 CTTCCGGATGGCACAGTGGATGGGACAAGGGACAGGAGCGACCAGCACATTCAGCTGCAG 218 121 CTTCCGGATGGCACAGGGATGGGACAAGGGACAGGACCACCAGCACATTCAGCTGCAG 180 219 CTCAGTGCGGAAAGCGTGGGGGAGGTCTATAAAAGAGTACCGAGACTGGCCAGTACTTG 278 Stegmann, T.J., Kordyum, V.A., Slavchenko, I.Yu., Chernykh, S.I. and 39 ATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCA Method of producing biologically active human acidic fibroblast 39 ATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCA 0; Gaps 446 408 Length 464; Length 468; 399 AAITGGTTTGTTGGCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCT growth factor and its use in promoting angiogenesis Patent: US 6642026-A 3 04-NOV-2003; Indels linear 0; Indels Score 408; DB 9; Le Pred. No. 5.7e-209; ó Pred. No. 5.7e-209; 63.9%; Score 408; DB 6; 100.0%; Pred. No. 5.7e-20 tive 0; Mismatches 0 DNA 0; Mismatches Sequence 3 from patent US 6642026. 468 bp /mol_type="genomic DNA" Location/Qualifiers /organism="unknown" 63.9%; S AR428605.1 GI:40188276 (bases 1 to 468) Matches 408; Conservative Matches 408; Conservative 1. .468 Query Match Best Local Similarity Unclassified. Vozianov, O.F. Similarity AR428605 Unknown. Unknown Query Match Best Local source DEFINITION ORGANISM ACCESSION REFERENCE JOURNAL RESULT 11 VERSION KEYWORDS AUTHORS AR428605 FEATURES TITE SOURCE ORIGIN LOCUS ò 셤 ò 셤 ò 유 à 셤 à .d ò a à g à g В ò ð ö ద

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3GGAATTACAAGAGCCCAAACTCCTCTACTGTAGCAACGGGGCCACTTCCTGAGGATC 158
                                                                                                                                    TITCCGGATGGCACAGTGGGATGGGACAAGGGACAGGACGACCAGCACATTCAGCTGCAG 218
                                                                                                                                                                                                              TCAGTGCGGAAAGCGTGGGGGGGTGTATAAAGAGTACCGAGACTGGCCAGTACTTG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear PAT 02-DEC-1994
                                                         ATGGCTGAAGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCA 98
                                                                                                                                                                                                                                                                                                       TGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGAAG 398
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63.9%; Score 408; DB 6; Length 8501; 100.0%; Pred. No. 4.5e-209;
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ides,J.C. and Abraham,J.A.
COMBINANT FIBROBLAST GROWTH FACTORS
ent: WO 8701728-A 13 26-MAR-1987;
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uence 13 from Patent WO 8701728.
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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August 24, 2004, 19:11:51; Search time 440 Seconds (without alignments) 6159.887 Million cell updates/sec 1 gaattcgggaacgcgccaca......cctgaatttgtaagcaactt 638 US-10-022-554A-3 tle: US-1 rfect score: 638 quence: n on:

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3: geneseqn2000s;*

4: geneseqn2001as;*

6: geneseqn2001as;*

7: geneseqn2003s;*

7: geneseqn2003s;*

8: geneseqn2003c;*

9: geneseqn2003c;* abase:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Aac66128 Mutant vo				' -			•				Address on ampli							Aac66130 Mutant FG
AAC66128	AAC66129	ADD68675	ADD68676	AAX81392	AAX81391	ADD68692	AAX81396	ADD68691	AAX81378	ADD68686	ADD68690	AAX81393	AAX81394	AAT45984	AAX81397	AAX81380	AAC66126	AAC66130
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54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	48.4	40.4	40.0	39.8	39.7
345	345	345	345	345	345	345	345	345	345	345	345	345	345	309	258	255	254	253
27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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enhancing the effectiveness of an FGF-1 response, or for stimulating FGF-1 response in a mammal. The present sequence is the mutant FGF-1

coding sequence

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Sequence 638 BP; 175 A; 164 C; 166 G; 133 T; 0 U; 0 Other;

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The present invention provides the protein and coding sequences of human fibroblast growth factor-1 (FGF-1) and a mutant that is resistant to thrombin degradation. The thrombin degradation resistant FGF-1 protein can be used for treating a disease or disorder (e.g. myocardial ischaemia, peripheral vascular disease, cerebral ischaemia, epithelial injury, epidermal wound injury, nerve injury, or bone damage), for
                                                                                                                                                                                            Thrombin resistant FGF-1, FGF-1, fibroblast growth factor-1, myocardial ischaemia; peripheral vascular disease; cerebral ischaemia; peripheral vandular disease; cerebral ischaemia; epithelial injury; epidarmal wound injury; nerve injury; mutant; bone damage; vasotropic, cardiant; cerebroprotective; vulnerary; neuroprotective; osteopathic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New thrombin degradation resistant fibroblast growth factor-1 (FGF-1) polypeptide, useful for treating a disease or disorder, e.g. cerebral ischemia or bone damage, or for enhancing the effectiveness of an FGF-1 response in a mammal.
                                                                                                                                                                Thrombin resistant FGF-1 mutant coding sequence.
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ALIGNMENTS
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/product= "FGF-1 mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "no start codon"
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                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                        ACF04029 standard; DNA; 638 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-DEC-2002; 2002WO-US039686.
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                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                         61 CCTTCACAGGCCCTGACGGAGAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAC 120
                                                                                                                           61 CCITCACAGCCCTGACCGAGAGTTIAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAC 120
                                                                                                                                                               121 TCCTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATG 180
                                                                                                                                                                                          121 recretacraracaacagagaccacrrecgagarecrrecgaragaracagagagarg 180
                                                                                                                                                                                                                     181 GGACAAGGGACAGGACCAGCACATTCAGCTGCAGCTCCAGTGCGGAAAGCGTGGGGGG 240
                                                                                                                                                                                                                                               181 GGACAAGGGACAGGAGCCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGG 240
                                                                                                                                                                                                                                                                            241 AGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTT 300
                                                                                                                                                                                                                                                                                                     241 AGGIGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGCTTT 300
                                                                                                                                                                                                                                                                                                                                 301 TATACGGCTCACAGACACCCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACC 360
                                                                                                                                                                                                                                                                                                                                                        1 GAATTICGGGAACGCGCCACAAGCAGCAGCTGCTGAGGCCATGGCTGAAGGGGAAATCACCA 60
                                                                       361 ATTACAACACCTATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGCCTCAAGA 420
                                                                                                                                                                                                                                                                                                                                                                                                          421 AGAATGGGAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 GITTCGAGGGTCCTCACCTGGTTGACCCCAAAAATGTTCCCTTGACCAITGGCTGCGCT 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 ICCCCCTGCCAGTCTCTGATTAAAGAGATCTGTTCTGGTGTTGACCACTCCAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 TCCCCCTGCCAGTCTCTTCTGATTAAAGATCTGTTCTGGTGTTGACCACTCCAGAGAA
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete cDNA sequence of human endothelial cell growth factor (ECGF).
                               ö
100.0%; Score 638; DB 8; Length 638; 100.0%; Pred. No. 1.8e-304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endothelial cell regeneration; blood vessel regeneration; ss.
                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601 AACCCCCAGGCCAGAGCCTGAATTTGTAAGGAACTT 638
                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Beta ECGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAN70788 standard; cDNA; 638 BP.
                          638; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
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 Query Match
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                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
CDS
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/product= "Acidic FGF"

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GITICGAGGGTCCTCACCTGGTTGACCCCAAAAATGTTCCCTTGACCATTGGCTGCGCT 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovine beta-endothelial cell growth factor (beta-ECGF, AAW03999) having a mol.wt. of 20 kD can be purified at least 16300 fold from bovine brain using heparin-Sepharose affinity chromatography. ECGF is useful for, among other purposes, diagnostic applications and has potential in the treatment of damaged blood vessels or other endothelial cell-lined structures. Human ECGF (AAT37503) or fragments may be obtained using oligonucleotides (AAT37504 and AAT37509 to AAT37509) whose design is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  based on the sequence of bovine alpha- and beta-ECGF. (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                          Endothelial cell growth factor; BCGF; blood vessel; regeneration;
heparin-Sepharose affinity chromatography; probe; oligonucleotide; FGF;
fibroblast growth factor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAATTICGGGAACGCGCCACAAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCA 60
                Isolated, purified, biologically active bovine beta endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth factor - useful to regenerate or treat damaged blood vessels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                 601 AACCCCCAGCCCACAGAGCCTGAATTTGTAAGCAACTT 638
                                                                                                         Ouery Match
Best Local Similarity 99.5%; Pred. No. 5.9e-229;
                                                                                                                                                                                                                                                                                                                                                                                                 Human beta-endothelial cell growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RHON ) RHONE POULENC RORER PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSDB; AAW04805, AAW04806, AAW04807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= c
/label= acidic_FGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= d
/label= alpha-ECGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/label= beta-ECGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 8; 28pp; English.
                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86US-00835594.
87US-00134499.
91US-00693079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-00334884.
                                                                                                                                                                                                                                        AAT37503 standard; DNA; 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-00799859.
                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .503
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                                                                                                                                                                                                                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maciag T, Burgess W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-412132/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAR-1986;
18-DEC-1987;
29-APR-1991;
                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                           29-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5552528-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-SEP-1996
                                                                                                                                                                                                                                                                                      AAT37503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc RNA
                                                                                                                                                                                               RESULT 3
                                                                                                                                                                                                                                                                                 $2 \times \times
                                        g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           To screen the human brain stem cDNA library for clones contg. ECGF inserts, a specific oligonucleotide was designed. This oligonucleotide was based upon a partial AA sequence analysis of the amino terminus of ECGF (see AAP70460 and AAP70461). Fig 3c sets forth for comparison the AA sequence of cyanogen bromide-cleaved bovine alpha and beta ECGF (AAP70834). The two clones that were isolated, ECGF clones 1 and 29, were analysed in further detail. The nucleotide sequence of these clones and the AA sequence deduced from the nucleot acid sequence is shown in Fig 8 (see AAN70788 and AAP70482). (Updated on 25-MAR-2003 to correct pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 TATACGGCTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 AGGIGIATATAAAAGAGTACCGAGACTGGCCAGTACTIGGCCATGGACACGGACGGGCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 ATTACAACACCTATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGCCTCAAGA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 AGAATGGGAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAATGGGAAGTTGCAAACGCGGTCCTCGGACTCACTATGGCCAGAAAGCAATCTTGTTTC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAATTCGGGAACGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATCCTTCCGGGATGGCACAGTGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 GGACAAGGGACAGGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human endothelial cell growth factor - produced by recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 5.9e-229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.0%; Score 485; DB 1;
99.5%; Pred. No. 5.9e-229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                        Jaye M, Burgess W, Maciag T, Drohan W;
                            /*tag= d
/product= "Alpha ECGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              techniques, useful for wound healing.
                                                                                                                                                                                                                                                                     (MELO-) MELOY LAB INC. (RORE ) RORER BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example, Fig 8; 43pp; English.
                                                                                                                                                                                   87WO-US000425.
                                                                                                                                                                                                                              86US-00835594.
       102. .506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   635; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1987-264128/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAP70482.
                                                                                                                                                                              02-MAR-1987;
                                                                                                                                                                                                                              03-MAR-1986;
                                                                                           WO8705332-A.
                                                                                                                                        11-SEP-1987.
    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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61 CCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAC 120
                                                                         121 TCCTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGGATG 180
                                                                                           181 GGACAAGGGACGAGGACCAGCACATTCAGCTGCAGGTGCGGAAAGCGTGGGGGG 240
                                                CCTTCACAGGCCCTGACGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGGCCCAAAG 120
                                                                                                                                            241 AGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTT 300
                                                                                                                                                                                                                                              241 AGGIGIATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGCCTTT 300
                                                                                                                                                                                                                              301 TATACGGCTCACAGACACCCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACC 360
                                                                                                                                                                                                                                                                                361 AITACAACACCTATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGCCTCAAGA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601 AACCCCCAGAGAGAGATTTGTAAGCAACTT 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human endothelial cell growth factor gene.
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29-APR-1991;
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This sequence represents the complete cDNA sequence encoding both human alpha— and beta-endothelial cell growth factors (ECGP, AAW75413-W75414). The sequence was isolated from a human brain stem cell cDNA library using a probe designed based on fragments of the bovine ECGF (see AAW75416.W75418). The ECGF protein can be used in compositions for promoting wound healing. ECGF is also used to grow cells on a prosthetic device

Compositions for promoting wound healing - containing endothelial cell growth factor polypeptides.

Example; Fig 8; 23pp; English.

Drohan WN;

Jaye M, Burgess W, Maciag T,

WPI; 1998-594032/50.

P-PSDB; AAW75415.

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                                                                                                                                                                        61 CCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAC 120
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                                                                                                                                                                                                                                                                            121 TCCTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATG 180
                                                                                                                                                                                             61 CCTTCACAGCCCTGACCGAGAGTTTAATCTGCCTCCAGGAATTACAAGAAGCCCAAAC 120
                                                                                                                                                                                                                                                                                                             181 GGACAAGGGACAGGACCAGCACATTCAGCTGCAGGTCCGGAAAGCGTGGGGGG 240
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                                                                                                                                      1 GAATICGGGAACGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGAAATCACCA 60
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                                                                                                     1 GAATTCGGGAACGCCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCA
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                                            DB 2; Length 638;
Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;
                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human endothelial cell growth factor (ECGF) cDNA sequence.
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                                      Score 485; DB 2; L
Pred. No. 5.9e-229;
                                                                         0; Mismatches
                                      76.0%;
99.5%;
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                                                                     Matches 635; Conservative
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                                                       Best Local Similarity
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                                      Query Match
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The invention relates to DNA encoding human endothelial cell growth factors (ECGF) and plasmids comprising the DNA sequences. The DNA encodes a cleavable signal peptide and an ECGF, where removal of the signal peptide yields a mature form of the ECGF, where the ECGF is alpha-ECGF or beta-ECGF. The DNA is used to produce recombinant ECGF proteins, which ò CCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAC 120 can be used in treatments to repair or regenerate blood vessels or other structures lined with endothelial cells. The present sequence represents a human ECGF cDNA sequence (determined from lambda ECGF clones 1 and 29) 61 CCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAC 120 TCCTCTACTGTAGGAGGAGGGAGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATG 180 DNA encoding a cleavable signal peptide and an endothelial cell growth factor - useful for producing recombinant endothelial cell growth factor 1 GAAITICGGGAACGCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGAAATCACCA 60 240 240 241 AGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTT 300 GAATTCGGGAACGCGCCACAAGCAGCAGCTGCTGAGCCATGAGGGGAAAATCACCA 60 181 GGACAAGGGACAGGAGCGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGG 0; Gaps /*tag* c /note= "acidic FGF begins at this position" "alpha-ECGF begins at this position" /*tag= b
/note= "beta-ECGF begins at this position" 76.0%; Score 485; DB 2; Length 638; Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other; 3; Indels regenerate; blood vessel; endothelial cell; human; ss. 5.9e-229; Pred. No. 5.9e 0; Mismatches Drohan WN; (RHON) RHONE-POULENC RORER PHARM INC. Location/Qualifiers /product= "ECGF" Disclosure, Fig 8, 23pp, English. Jaye M, Burgess W, Maciag T, 87US-00134499. 91US-00693079. 91US-00799859. 97US-00840088 86US-00835594. 94US-00334884. 96US-00743261. 95US-00472964 99.5%; ĸ .506 635, Conservative /*tag≂ /*tag≃ WPI; 1999-069734/06. Local Similarity P-PSDB; AAW92291 Homo sapiens. misc_feature misc_feature misc feature 11-APR-1997; US5849538-A. 29-APR-1991; 03-NOV-1994; 15-DEC-1998 18-DEC-1987; 27-NOV-1991; 04-NOV-1996; 07-JUN-1995 proteins. 19 121 Query Match Matches Key Š 셤 g g à ò ò ద à 유

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TATACGGCTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACC 360
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                                                          361 ATTACAACACCTATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGCCTCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New thrombin degradation resistant fibroblast growth factor-1 (FGF-1) Polypeptide, useful for treating a disease or disorder, e.g. cerebral ischemia or bone damage, or for enhancing the effectiveness of an FGF-1 response in a mammal.
                                                                                                                       421 AGAATGGGAGCTGCAAACGCGGTCCTAAAACTCACTATGGCCAGAAAGCAATCTTGTTTC
                                                                                                                                                                                  481 TCCCCCTGCCAGTCTTCTGATTAAAGAGATCTGTTCTGGTGTTGACCACTCCAGAGAA
                                                                                                                                                                                                                 481 TCCCCCTGCCAGTCTTCTGATTAAAGAGATCTGTTCTGGTGTTGACCACTCCAGAGAA
                                                                                                                                                                                                                                               541 GITTCGAGGGTCCTCACCTGGTTGACCCCAAAAATGTTCCCTTGACCATTGGCTGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myocardial ischaemia, peripheral vascular disease; cerebral ischaemia,
epithelial injury; epidermal wound injury; nerve injury; bone damage;
vasotropic; cardiant; cerebroprotective; vulnerary; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombin resistant FGF-1 mutant production wildtype coding sequence.
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                                                                                                                                                                                                                                                                                                                                   601 AACCCCCACACACACACATTTGTAAGCAACTT 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "FGF-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-DEC-2002; 2002WO-US039686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-2001; 2001US-00022554.
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/product= "
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injury, epidermal wound injury, nerve injury, or bone damage), for enhancing the effectiveness of an FGF-1 response, or for stimulating an FGF-1 response in a mammal. The present sequence is the wildtype FGF-1
                                                                                                                                                                                                                                                                                                                                  181 GGACAAGGGACAGGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGG
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                                                                                                    Length 638;
                                                                     Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;
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99.5%; Pred. No. 5.9e-229;
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                                                                                                                                     Matches 635; Conservative
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                                                                                                             Best Local Similarity
                                          coding sequence
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A cDNA clone (AA745985) codes for human endothelial cell growth factor (AAW66818). To obtain the clone, a human brain stem cDNA library was screened with a probe (see also AA745986) hased on N-terminal sequences of bovine ECGF (see also AA745986). ECGF clones 1 and 29 were flanking regions sequenced by the chain termination method. DNA sequences (see also AA74598-84) derived from the complete cDNA can be used in the large-scale prodn. of recombinant ECGF beta (AAM66816) and alpha (AAW66817) in transformed host cells. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                 Recombinant human endothelial cell growth factors - for treating damaged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 GCTGAAGGGAAATCACCACCTTCACAGCCTGACCGAGAAGTTTAATCTGCCTCCAGGG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 GCTGAAGGGAAATCACCACTTCACAGCCTGACGGGAAGTTTAATCTGCCTCCAGGG 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 AIGGACACCGACGGCTTTIAIACGGCTCACAGACACCAAATGAGGAATGITTGTTCCTG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 GAAAGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGAAGAAT 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      402 TGGTTTGTTGGCCTCAAGAAGGAATGGGAAGCTGCAAACGCGGTCCTAAAACTCACTATGGC 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             522 TGTTGACCACTCCAGAGAAGTTTCGAGGGTCCTCACCTGGTTGACCCCAAAAATGTTCC 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 CCGGATGGCACAGTGGATGGGACAAGGGACAGGAGCGACCAGCACATTCAGCTGCAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 AATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               582 CITGACCAITGGCIGCGCTAACCCCCAGCCCAGAGCCIGAAITTGIAAGCAACIT 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 639 BP; 172 A; 165 C; 168 G; 134 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1e-208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 444;
                                                                                                                                                                            Burgess
                                                                                                                                        (RHON ) RHONE POULENC RORER PHARM INC.
                                                                                                                                                                                                                                                                                                  Example D; Fig 8; 22pp; English.
                                                                                                                                                                       Drohan WN, Jaye M, Maciag T,
                                                            87US-00134499.
                95US-00472964.
                                               86US-00835594
                                                                                            91US-00799859.
                                                                                                            94US-00334884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.6%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 594; Conservative
                                                                                                                                                                                                     WPI; 1996-505421/50.
                                                                                                                                                                                                                                                                  blood vessels, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                      P-PSDB; AAW06818
                07-JUN-1995;
                                                                            29-APR-1991;
                                                                                            27-NOV-1991;
03-NOV-1994;
                                                              18-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           field.)
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AAN93088 standard; DNA; 638 BP.

AAN93088

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence encodes human acidic fibroblast growth factor (aFGF). See also AAN93087 and AAN93089. (Updated on 25-WAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 GCGCCACAAGCAGCTGCTGAGCCATGGCTGAAGGGAAATCACCACCTTCACAGCCC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 IGACCGAGAAGITITAATCTGCCTCCAGGGAAITACAAGAAGCCCCAAACTCCTCTACTGTA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 GCAACGGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGGACAAGGGACA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 GGAGCGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGAGGTGTATATAA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 GGAGCGACCAGCACATTCAGCTGCAGCTCAGTGCGAAAGCGTGGGGGAGGTGTATATAA 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 AGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCATTACAACACT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant DNA encoding new fibroblast growth factor analogues - useful e.g. for accelerating wound healing and to control neovascularisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 AGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCATTACAACACCT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 GCGCCACAAGCAGCAGCTGCTGAGGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                         /*tag= a
/label= human acidic fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.0%; Score 434; DB 1; Length 638; 100.0%; Pred. No. 8.7e-204; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 638 BP; 170 A; 156 C; 168 G; 144 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                            Acidic fibroblast growth factor; ss.
                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               Protter A;
                                                                   Acidic fibroblast growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 2; 44pp; English.
                                                                                                                                                                                                                                                                  88EP-00306158.
                                                                                                                                                                                                                                                                                           87US-00070797.
                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAAACGCGGTCCT 446
                                                                                                                                                                                                                                                                                                                 (BIOU ) BIOTECH RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 434; Conservative
                                                                                                                                                                                                                                                                                                                                           Fiddes JC, Abraham JA,
                                                                                                                                                                                                                                                                                                                                                                    WPI; 1989-009785/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAN93087.
                                                                                                                                                                                                                                                                 06-JUL-1988;
                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                          07-JUL-1987;
                             25-MAR-2003
25-JUN-1990
                                                                                                                                                           mat_peptide
                                                                                                                                                                                                                                       11-JAN-1989.
                                                                                                                                                                                                                EP298723-A.
     AAN93088;
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Composition useful for identifying modulators of fibroblast growth factor-mediated signaling for use in treating cancer, has ternary complex of FGF-receptor, FGF ligand and heparin agonist or antagonist.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 GCGCCACAAGCAGCAGCTGATGCCTGAAGGGGAAATCACCACCTTCACAGCCC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 GCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGGTGGATGGGACAAGGGACA 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 AGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTCAC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to an isolated composition comprising a ternary complex of an Fibroblast Growth Factor (FGF) ligand polypeptide (ABR5G1G3, ABR5G1G5), an FGF receptor polypeptide (ABR5G1G4) and a heparin agonist or antagonist, where the agonist or antagonist binds to the FGF ligand polypeptide and the FGF receptor polypeptide to form the ternary complex. The composition is useful for identifying a compound that is an inhibitor of FGF receptor activity. FGF1 is also known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 GCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                   Human, Fibroblast Growth Factor 1; FGF1; acidic FGF; aFGF; acidic Fibroblast Growth Factor; protein co-ordinate data; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2357 BP; 691 A; 521 C; 567 G; 578 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                            Human Fibroblast Growth Factor 1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 68.0%; Score 434; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 8.4e-204;
Matches 434; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Fig 16B; 288pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "FGF1"
      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moosa M, Green DL, Linhard RJ;
ACC42968 standard; DNA; 2357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2002; 2002WO-US034986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2001, 2001US-0335583P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYNY ) UNIV NEW YORK STATE.
                                                                                                                   18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         142. .609
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003038054-A2.
                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAY-2003.
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313 AGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGGAGCATTACAACACT 372
              373 ATATATCCAAGAAGCATGCAGAAGAATTGGTTTGTTGGCCTCAAGAAGAATGGGAGCT 432
                                                               433 GCAAACGCGGTCCT 446
                                                                                                             536 GCAAACGCGGTCCT 549
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was obtained in electronic format directly from USPTO at

ABX63225 standard; cDNA; 4087 BP. (first entry) 25-FEB-2003 ABX63225; RESULT 10 ABX63225

Human cDNA #225 differentially expressed in activated vascular tissue.

Human, gene, ss, vascular tissue, cytostatic, atherosclerosis, cardiant, hypotensive, antidiabetic, gynaecological, vasotropic, cerebroprotective, gene therapy, vascular disease, cancer, coronary, artery disease, hypotrension, diabetes, pre-eclampsia, restenosis, ischaemia-reperfusion injury, stroke.

Homo sapiens.

US2002137081-A1.

26-SEP-2002.

08-JAN-2002; 2002US-00044090.

28-JUL-2000; 2000US-0222469P. 08-JAN-2001; 2001US-0260483P.

(BAND/) BANDMAN O.

Bandman O;

WPI; 2003-110597/10.

Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several CDNAs that are differentially expressed in activated vascular tissue.

Claim 1; Page; 18pp; English.

This invention relates to a combination comprising several cDNAs that are differentially expressed in activated vascular tissue. The invention also discloses a high throughput method for detecting differentially expressed concloses a high throughput method for detecting may have antiarteriosclerotic, cytostatic, cardiant, hypotensive, antidiabetic, gynaecological, vasotopic and exerbroprotective activities and may be used in gene therapy. The CDNAs of the invention may be used in a high-throughput methods for detecting differential expression of one or more compute methods for detecting differential expression of one or more throughput methods for detecting differential expression of the invention. A protein encoded by the cDNA may be used to screen several conceutes or compounds to identify a ligand that specifically binds to the protein or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or the protein from a sample. The nucleotides may be useful for diagnoshing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. altersoclerosis, can also be used for large-scale injury, restension, diabetes, pre-eclampsia, ischaemia-reperfusion analytic of an allery expression and also an also be used for large-scale analytic or annealytic or an also be used for large-scale. genetic or gene expression analysis of several new nucleic acid molecules. Antibodies to the proteins encoded by the CDNAs are useful for diagnosing pre-pathologic disorders, and chronic or acute diseases associated with abnormalities in the expression, amount or distribution of the protein. The present sequence represents a CDNA of the invention that is differentially expressed in activated vascular tissue. Note: The sequence data for this patent did not form part of the specification, but

Inhibiting expression of target gene, useful e.g. for inhibiting oncogenes, by administering double-stranded RNA complementary to the

Claim 10; Page 147; 203pp; German.

oncogenes, by administering dov target and having an overhang.

Hadwiger P;

Rost S,

Kreutzer R, Limmer S, (RIBO-) RIBOPHARMA AG.

WPI; 2002-590671/63.

09-JAN-2001; 2001DE-01000586. 26-OCT-2001; 2001DE-01055280.

29-NOV-2001; 2001DE-01058411.

07-DEC-2001; 2001DE-01060151

09-JAN-2002; 2002WO-EP000152.

WO200255693-A2. Homo sapiens.

18-JUL-2002.

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                                                                                                                      73 TGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTATA 132
                                                                                                                                                                                                        133 GCAACGGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGGGACAAGGGACA 192
                                                                                                                                                                                                                      660 GGAGCGACCAGCACTTCAGCTGCAGCTCCGGAAAGCGTGGGGGGAGCTGTATATAA 719
                                                                                                                                                                                                                                                         GGAGCGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGGAGGTGTATATAA 252
                                                                                                                                                                                                                                                                                                       253 AGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTCAC 312
                                                                                                                                                                                                                                                                                                                             720 AGAGTACCGAGACTGGCCAGTACTTGGCCATGGACGCGACGGGCTTTTATACGGCTCAC 779
                                                                                                                                                                                                                                                                                                                                                      313 AGACACCCAAATGAGGAATGTTTGTTCCTGGAAGGCTGGAGGAGAACCATTACAACACT 372
                                                                                                                72
                                                                                                                                                                                                                                                                                                                                                                              780 AGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCATTACAACACCT 839
                                                                                                                                                                                                                                                                                                                                                                                                            432
                                                                                                                                                                                                                                                                                                                                                                                                                  RNA inhibition, dsRNA1; gene expression inhibitor, oncogene; cytostatic, virucide; protozoacide; gene; ds.
                                                                                                           13 GCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCC
                                                                                                                                                                                 540 TGACCGAGAAGTITAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTA
                                                                                                                                                                                                                                                                                                                                                                                                     373 ATATATCCAAGAAGCATGCAGAGAAGTTGGTTTGTTTGGCCTCAAGAAGAATGGGAGCT
                                                                                        Gaps
                                                                                       0
                                    Sequence 4087 BP; 1164 A; 886 C; 959 G; 1078 T; 0 U; 0 Other;
                                                              Length 4087;
                                                                                      0; Indels
             http.seqdata.uspto.gov/sequence.html?DocID=20020137081
                                                            Score 434; DB 7; Le
Pred. No. 8.3e-204;
                                                                  100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABV78179 standard; DNA; 468 BP.
                                                             68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      433 GCAAACGCGGTCCT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             900 GCAAACGCGGTCCT 913
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                                                                                   Matches 434; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human DNA SEQ ID NO 63.
                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-NOV-2002
                                                            Query Match
                                                                                                                                                                                                                                                        193
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The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (asl) of dsRNA1 is complementary to (I) and at least one end of dsRNA1 has an overthang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. in humans, also genes in Plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into dsRNA1 greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of a gene related to the invention

Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 Other;

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99 GGGAATTACAAGAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 158
                                                                                                                                                      61 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 120
                                                                                                                                                                                   159 CTTCCGGATGGCACAGTGGGACAAGGGACAGGAGCGACCAGCACATTCAGCTGCAG 218
                                                                                                                                                                                                     219 CTCAGTGCGGAAAGCGTGGGGGGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTG 278
                                                                                                                                                                                                                                                                      1 ATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCA 60
                                                                                                                                                                                                                                                                                                                                                                         339 CTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGGAAG 398
                                                                   98
                                                         39 ATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCA
                                   ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                          399 AAITIGITIGITIGGCCICAAGAAGAAIGGGAGCTGCAAACGCGGICCI 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 AATTGGTTTGTTGGCCTCAAGAATGGGAGCTGCAAACGCGGTCCT 408
   Length 468;
                                0; Indels
Match 63.9%; Score 408; DB 6;
Local Similarity 100.0%; Pred. No. 6e-191;
                                0; Mismatches
                           Matches 408; Conservative
Query Match
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protozoacide; gene expression; antisense; tumour; infection; Plasmodium;
virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Double stranded RNA, dsRNA, RNAi, RNA inhibition, cytostatic, virucide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus; human papilloma virus; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rost S, Hadwiger P;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 63.
                                                                                                  ABZ35755 standard; DNA; 468 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JAN-2001; 2001DE-01000588.
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                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RIBO-) RIBOPHARMA AG.
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                                                                                                                                                                                                                ABZ35755;
RESULT 12
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                                                                                                                                                                                                           ACCOUNT OF THE SECTION OF THE SECTIO
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Inhibiting expression of target genes, useful e.g. for treating tumors, by introducing into cells two double-stranded RNAs that are complementary
                                                                                                    to the target.
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Claim 13; Page 44; 100pp; German.

method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNA1). The method is particularly used to treat tumours or infections, especially by Plasmoddum or vitroses/vitroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonucleotides (GSRNAI and II), both with a double-stranded (GS) structure of at most 49 sequential mucleotide pairs. At least part of one strand (S1, S2) of the ds structures in each of dsRNAI and II are complementary to regions in the target gene. The interferon. The present sequence is that of a target DNA of the invention

DB 6; Length 468; Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 Other; 100.0%; Preu. ... Score 408; 63.9%; Query Match

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Gaps ٥;

0; Indels

Pred. No. 6e-191;

408; Conservative Local Similarity

Matches

99 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 158 61 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 120 218 1 ATGGCTGAAGGGGAAATCACCACCTTCACAGCCTGACGGAGAAGTTTAATCTGCCTCCA 60 39 AIGGCIGAAGGGGAAAICACCACCIICACAGCCCIGACCGAGAAGIIITAAICIGCCICCA 98 159 ò g õ 셤 à 셤

CTCAGTGCGGAAAGCGTGGGGGGGGTGTATATAAAGAGTACCGAGGACTGGCCAGTACTTG 278 181 CICAGIGCGGAAAGCGIGGGGGGGGGTGIAIAAAGAGIACCGAGACTGGCCAGIACTIG 219 ò g

339 CTGGAAAGGCTGGAGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGAAG 398 Š 임 à

399 AATTGGTTTGGTGCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCT 446 361 ò g

301 CTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGGAAG 360

g

ABX09998 standard; DNA; 468 BP. Human DNA fragment SEQ ID 63. (first entry) 23-JAN-2003 ABX09998; RESULT 13 ABX09998 ü N X E ğ

Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental; prion; inhibition; human; ds.

09-JAN-2001; 2001DE-01000587. DE10100587-C1. Homo sapiens. 21-NOV-2002.

09-JAN-2001; 2001DE-01000587.

WPI; 2002-683450/74.

ABL91720 standard; DNA; 468 ABL91720 임 田は à 셤 ò g ò g ò 엄 ò g Dp ò target gene by introducing into the cell that contains the target gene at least one oligoribonucleotide (dsRNAI) that has a double-stranded (ds) pathogenic organisms (particularly plasmodia) or in viruses or viroids (pathogenic in humans, animals or plants). Treating the cells with interferon greatly increases the extent to which dsRNA can inhibit expression of the target genes, and the effect is even greater when dsRNA are modified to increase their stability. ABX09936-ABX10075 represent gene fragments used to illustrate the method of the invention 99 GGGAATTACAAGAAGCCCAAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 158 61 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 120 121 CTTCCGGATGGCACAGTGGGATGGGACAGGGGCACCAGCACCAGCACTGGCAG 180 219 CTCAGTGCGGAAAGCGTGGGGAGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTG 278 CITCCGGATGGCACAGGGACAAGGGACAGGAGGAGCAACAGCACATTCAGCTGCAG 218 301 CTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGAAGCATGCAGAAAG 360 double-stranded oligoribonucleotide, after 339 CTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGAAG 398 39 AIGGCIGAAGGGGAAAICACCACCTICACAGCCCTGACCGAGAAGTITAAICTGCCTCCA 98 1 ATGGCTGAAGGGGAAATCACCACCTTCACAGCCTGACCGAGAAGTTTAATCTGCCTCCA 60 least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before introduction of dsRNAI. The method is used to inhibit expression of target genes, particularly oncogenes, cytokine genes, Id (not defined) protein genes; developmental or prion genes, or genes expressed in invention describes a novel method for inhibiting expression of a structure of not more than 49 consecutive nucleotides (nt), where at 0; Gaps Inhibiting expression of target genes, e.g. oncogenes, in cells, by Human acidic fibroblast growth factor; phage T7 polymerase promoter; lysis; phage dependent superproduction; FGF fr HUMECGFB; gene; ds. 399 AAITGGTTTGTTGGCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCT 446 361 AATTGGTTTGTTGGCCTCAAGAAGAATGGCAGCTGCAAACGCGGGTCT 408 63.9%; Score 408; DB 6; Length 468; Human acidic fibroblast growth factor DNA - FGF fr HUMECGFB. 0; Indels Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 Other; Pred. No. 6e-191; Hadwiger P; 0, Mismatches treating the cell with interferon. Disclosure; Page 49; 98pp; German. Rost S, introduction of complementary AAK98918 standard; DNA; 468 BP. Best Local Similarity 100.0%; Matches 408; Conservative (first entry) Limmer S, (RIBO-) RIBOPHARMA AG. WPI; 2002-742209/81 target gene by Kreutzer R, 24-MAY-2002 Homo sapiens 159 AAK98918; Query Match RESULT 14 AAK98918 à 임 ð g ò g ò 셤 à g à 셤 à g

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Bacteriophage-dependent method for producing biologically active proteins or peptides, involves employing an Escherichia coli transformed with a plasmid containing the targeted gene(s) operably linked to a promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biologically active protein comprising infecting a strain of Escherichia coli, which has been transformed with a plasmid having at least one copy of an expressible gene, such as a human acidic fibroblast growth factor. The expressible gene encodes a biologically active protein operably linked to a plage T7 polymerase promoter, with a bacteriophage capable of mediating delayed lysis. The method is useful for the phage dependent superproduction of biologically active protein and peptides. The method is particularly useful for enhancing the production of heterologous proteins in bacterial host cells. This polymorleotide sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGGCCACTTCCTGAGGATC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 CTCAGTGCGGAAAGCGTGGGGGAGGTGTATAAAGAGTACCGAGACTGGCCAGTACTTG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CTCAGTGCGGAAAGCGTGGGGGGGTGTATAAAGAGTACCGAGACTGGCCAGTACTTG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 AIGGCIGAAGGGGAAAICACCACCIICACAGGCCCIGACCGAGAAGIIIAAICIGCCIICCA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the DNA of a human acidic fibroblast growth factor - FGF fr HUMECGFB of
                         /*tag= a
/product= "Protein of human acidic fibroblast growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 CHICCGGAIGGCACAGTGGAIGGGACAAGGGACAGGGGGACCAGCACAHTCAGCTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for enhancing the production of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.9%; Score 408; DB 6; Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Kordyum VA, Chernykh SI, Slavchenko IY, Vozianov OF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 36-37; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                        (PHAG-) PHAGE BIOTECHNOLOGY CORP.
                                                                           factor (155AA)"
                                                                                                                                                                                                                                                                                                                15-AUG-2000; 2000US-0225437P.
                                                                                                                                                                                                                                                       15-AUG-2001; 2001WO-US025477.
122. .589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-269184/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAO19990
                                                                                                                                         WO200214468-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
                                                                                                                                                                                               21-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339
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Location/Qualifiers

Key

The invention relates to a method for inhibiting expression of a target gene (Rb19168-ABL91797) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single stranded segment of 1-4 nt. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the uppaired overhang increases stability and thus intracellular concentration Human, HIV; HCV; gene expression, oligoribonucleoride; tumour; pathogen; Plasmodium; virus; viroid; cytokine; prion, antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds. in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cytokine, Id, developmental or prion genes. Inhibiting gene expression in cells, useful for e.g. treating tumors, by introducing double-stranded complementary oligoRNA having unpaired Hadwiger P; Human polynucleotide SEQ ID NO 63. Claim 13; Page 47; 104pp; German. Rost S, 09-JAN-2001; 2001DE-01000586. 09-JAN-2001; 2001DE-01000586. 28-MAY-2002 (first entry) Limmer S, (RIBO-) RIBOPHARMA AG. WPI; 2002-270454/32. DE10100586-C1. Homo sapiens. 11-APR-2002. Kreutzer R,

39 AIGGCTGAAGGGGAAAICACCACCTICACAGGCCTGACCGAGAAGITITAAICTGCCICCA 98 0; Gaps 0; Indels 6e-191; 0; Mismatches Pred. No. 100.001 Matches 408; Conservative Query Match Best Local Similarity 61 à

159 CTTCCGGATGGCACAGTGGATGGGACAAGGGACAGAGGGGGACCAGATTCAGCTGCAG 218 99 GGGAATTACAAGAAGCCCAAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 158 219 CTCAGTGCGGAAAGCGTGGGGGAGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTG 278 CTCAGTGCGGAAAGCGTGGGGGGGGTGTATATAAAGAGTACCAGAACTGGCCAGTACTTG 240 241 GCCATGGACCGACGGGCTTTTATACGGCTCACAGACACCAAATGAGGAATGTTGTTC 300 CTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGAAG 398 399 AATIGGITITGITIGGCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCT 446 181 339 à g g à g ð ò g 임 à 셤 à

Search completed: August 24, 2004, 21:07:54 Job time : 443 secs

ABL91720;

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

(without alignments)
4116.961 Million cell updates/sec August 24, 2004, 20:52:07 ; Search time 86 Seconds Run on:

US-10-022-554A-3 Perfect score:

l gaattcgggaacgcgccaca......cctgaatttgtaagcaactt 638 Sequence:

OLIGO_NUC Gapop 60.0 , Gapext 60.0 Scoring table:

682709 seqs, 277475446 residues Searched:

0 Word size :

1365418 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Issued_Patents_NA:* Database :

1: /cgn2_6/ptodata/2/ina/5a_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5a_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6a_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6a_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/FGCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/ina/backfiles1.seg:

SUMMARIES

Result

63.9%; Score 408; DB 6; Length 468;

Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 Other;

DB ID Description	3 US-09-098-628-3 Sequence 3. Aproli	-655-1390 Sequence	Sequence	, H	د				-14 Seguence 14.	্ৰ	'n	Seguence	00	2	4	1	55.1	_	-3 Semience 3	1 Seguence 1.		Sequence 2,	Sequence 2, Sequence 1,	Sequence 2, Sequence 1, Sequence 3,	Sequence 2, A Sequence 1, A Sequence 3, A Sequence 3, A	Sequence 2, Sequence 1, Sequence 3, Sequence 3, Sequence 15, Sequence 16,	Sequence 2, Sequence 1, Sequence 3, Sequence 15, Sequence 15,	Sequence 2, Sequence 1, Sequence 15, Sequence 15, Sequence 25, Sequence 25,	Sequence 2, Sequence 1, Sequence 3, Sequence 16, Sequence 25, Sequence 25, Sequence 25,
	638	490	468	8501	454	197	450	454	454	630	270	44	44	44	44	44	261	465	465	465		465	465	465 465 465	465 465 465 471	465 465 465 471 477	465 465 465 471 477 59	465 465 471 477 59	465 465 471 471 59 59
Match Length DB	0.89	65.5	63.9	63.9	29.5	27.0	18.5	12.1	12.1	4.1	3.8	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	4	,	3.6	. w w	. w w w 5				
Score	434	418	408	408	186	172	118	77	77	56	24	23	23	23	23	23	23	23	23	23	23		23	23	23 23 23 23	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	23 23 23 21	23 23 21 21 21 21	23 23 23 21 21 21
No.	1	7	m	4	'n	9	7	œ	σ	10	7	12	13	14	12	16	17	18	19	20	51		22	23	223	23 24 25	22 23 24 26 26	22 23 24 25 27	22 23 24 25 27 28

09 73 TGACCGAGAAGTITTAATCTGCCTCCAGGGAATTACAAGAAGCCCCAAACTCCTCTACTGTA 132	QY 253 AGAGTACCGAGACTGGCCATGGACATGGACATGGACCACGAGGGCTTTTATACGCTCAC 312 Bb 305 AGATACCGAGACTGGCCATGGCCATGGACACCGACGGTTTTTATACGGCTCAC 364 QY 313 AGACACAAATGAGGATTGTTTTTTTTCTCGAGAAGCGTGGAGAACCATTACAACAC 372		RESULT 2 US-09-023-655-1390 ; Sequence 1390, Application US/09023655 ; Patent No. 6607879 ; GENERAL INFORMATION: ; APPLICANT: Cocks, Benjamin G. ; APPLICANT: Susan G. Stuart ; APPLICANT: Jeffery J. Seilhamser ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE ; NIMBER OF SEQUENCE: 100 PROPERTION FOR THE DETECTION OF BLOOD CELL GENE	CORRESPONDENCE ADDRESSE ADDRESSEE: INCTTE FORTER STREET: 3174 PORTER CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA CONTUTER READABLE FORM MEDIUM TYPE: FLOPPY MEDIUM TYPE: READPY COMPUTER: IBM PC CO OPERATING SYSTEM: P SOFTWARE: WOO'D PER	NI	; SEQUENCE CHARACTERISTICS: ; LENGTH, 490 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear ; IMMEDIATE SOURCE: ; TABARY CEMBANE
. 521 . 521 . 521 . 26, . 159, . 159, . 159, . 208, . 22, . 22, . 22, . 22, . 22, . 22, . 22, . 208,	Sequence 202, App Sequence 2657, Ap Sequence 1. Appli Sequence 16, Appl					Length 638; , Indels 0; Gaps 0;
	AT 4 US-09-670-134-202 461 4 US-09-621-976-2657 526 4 US-09-479-313B-1 528 4 US-09-479-313B-16 ALIGNMENTS	m US/09098628 J.C.	NVENTION: HUMAN BASIC FIBROBLAST GROWTH NVENTION: PACTOR ANALOG SEQUENCES: 69 SEVER ADDRESS: E: MORRISON & FOERSTER 755 PAGE MILL ROAD CA USA USA USA EXDABLE FORM:	OPERATING SYSTEM: Windows OPERATING SYSTEM: Windows OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0b RRENT APPLICATION DATA: APPLICATION NUMBER: US/09/098,628 CLASSIFICATION DATA: 10R APPLICATION DATA: FILING DATE: TORNEY/AGENT INFORMATION: TORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 131941	ET NUMBER: 21900-20089.10 N INFORMATION: 194-0792 ID NO: 3: RISTICS: see pairs acid double an .ng Sequence555	Score 434, DB 3; Le Pred. No. 6.3e-217; D; Mismatches 0;
30 20 3.1 C 31 20 3.1 C 32 18 2.8 34 18 2.8 35 18 2.8 36 18 2.8 37 18 2.8 37 18 2.8 37 18 2.8 40 17 2.7 C 41 17 2.7	44 44 45 17	ESUL S-09 Seq Pat GE	TITLE OF I TITLE OF I TITLE OF I NUMBER OF CORRESPOND ADDRESSES STREET: CITY: P STRIE: COUNTRY: ZIP: 94 COMPTER K MEDIUM I	AT PR	REFERENCE/DOCKET NUMBER: 21; TELECOMMUNICATION INFORMATION: TELEPHONE: 650-813-5600 TELERAX: 650-894-0792 TELE	US-09-098-628-3 Query Match Best Local Similarity 100 Matches 434; Conservative

65.5%; Score 418; DB 4; Length 490; ; STRANDEDNESS: single ; TOPOLOGY: linear ; IMMEDIATE SOURCE: ; LIBRARY: GENBANK ; CLONE: G396163 US-09-023-655-1390 Query Match

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339 CTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCAAGAAGCATGCAGAGAAG 398 399 AAITGGTTTGTTGGCCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCT 446 361 AAITGGTTTGTTGGCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCT 408 셤 ò à a 181 TCACTGCAGCTCAGTGCGGAAAGCGTGGGGGGGGTGTATATAAAGAGTACCGAGACTGG 240 29 CTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAA 88 1 CTGCTGAGCCATGGCTGAAGGGAAATCACCACCTTCACAGGCCCTGACCGAAGTTTAA 60 89 TCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGCCACTT 148 61 TCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTT 120 149 CCTGAGGATCCTTCCGGATGGCACAGTGGATGGGACAGGGACAGGAGCGACCAGCACAT 208 209 TCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGGGGGTGTATAAAAGAGTACCGAGACTGG 268 269 CCAGTACTTGGCCATGGACACCGACGGCTTTTATACGGCTCACAGACACCAAAATGAGGA 328 241 CCAGTACTTGGCCATGGACACCGACGGCTTTTATACGGCTCACAGACACCCAAATGAGGA 300 ò 99 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGGCCACTTCCTGAGGATC 158 159 CTTCCGGATGGCACAGTGGATGGGACAAGGGACAGGAGGACCAGCACATTCAGCTGCAG 218 121 CTTCCGGATGGCACAGTGGATGGGACAAGGACAGGACCACACCACATTCAGCTGCAG 180 219 CTCAGTGCGGAAAGCGTGGGGGGGGTGTATAAAAGAGTACCGAGACTGGCCAGTACTTG 278 86 1 AIGGCIGAAGGGAAAICACCACCTICACAGCCCTGACCGAGAAGTITAATCTGCCTCCA 60 389 TGCAGAGAAGAATTGGTTTGTTGGCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCT 446 361 TGCAGAGAAGAATTGGTTTGTTGGCCTCAAGAAGAATGGGGAGCTGCAAACGCGGTCCT 418 0; Gaps 39 ATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACGGAGAAGTTTAATCTGCCTCCA 0; Indels 0; Gaps 63.9%; Score 408; DB 4; Length 468; 100.0%; Pred. No. 2.4e-203; Best Local Similarity 100.0%; Pred. No. 1.4e-208; APPLICANT: Chernykh, Svitlana I.
APPLICANT: Slavchenko, Iryna Yu.
APPLICANT: Slavchenko, Iryna Yu.
APPLICANT: Slavchenko, Iryna Yu.
TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
TITLE OF INVENTION: STBROBLAST GROWTH FACTOR 155
CURRENT APPLICATION NUMBER: US/09/929,945
CURRENT FILING DATE: 2001-08-15 100.0%; Pred. ... SOFTWARE: FastSEQ for Windows Version 4.0 ; Sequence 3, Application US/09929945 ; Patent No. 6642026 APPLICANT: Stegmann, Thomas APPLICANT: Kordyum, Vitaliy A. 408; Conservative NUMBER OF SEQ ID NOS: 8 ORGANISM: Homo sapiens Best Local Similarity Matches 408; Conserv GENERAL INFORMATION: US-09-929-945-3 LENGTH: 468 US-09-929-945-3 TYPE: DNA SEQ ID NO 3 Query Match 19 셤 à ò qq à å ò g à 셤 à g à g à ò g ò d ò a ò 엄

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96 CCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 GACACCGACGGCTTTTATACGGCTCACAGACACCAAATGAGGAATGTTTCTTCCTGGAA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 AGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGAAGTT 402
                                                                             156 ATCCTTCCGGATGGCACAGTGGATGGGACAAGGGACAGGAGCGACCAGCACA 207
                                                                                                 APPLICANT: Florkiewicz, Robert Z.
APPLICANT: Balard, J. Andrew
TITLE OF INVENTIONS: INHIBITORS OF LEADERLESS PROTEIN EXPORT
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.5%; Score 118; DB 6; Length 450;
100.0%; Pred. No. 7.4e-52;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                       APPLICANT: ICHIMORI, YUZO; KONDO, KOICHI; IGARASHI, KOICHI;
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MONOCLONAL ANIBODY AGAINST AN ACIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                 FGF PROTEIN AND HYBRIDOMA FOR ITS PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: No. 6083706tenburg Ph.D., Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 760100.418C1
                                                                                                                                                                                                                                                                                                                                  CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/26,257
FILING DATE: 04-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 588,343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/030,613
FILING DATE: 25-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 14, Application US/09030613; Patent No. 6083706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 454 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                   ;Patent No. 5437995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 450
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                                                                                                                                                                                                                                                             ; SENDO, MASAHARU
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          339 CTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGAAG 398
                                    159 CTICCGGAIGGCACAGIGGAIGGGACAGGGACAGGAGCGACCAGCACATICAGCIGCAG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 CTTCCGGATGGCACAGTGGATGGGACAAGGGACCAGCACCAGCACTTCAGCTGCAA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 CTCAGTGCGGAAAGCGTGGGGGAGGTGTATAAAGAGTACCGAGACTGGCCAGTACTTG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 CTCAGTGCGGAAAGCGTGGGGGGGGGTGTATAAAGAGTACCGAGACTGGCCAGTACTTG 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 GCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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0
                                                                                                            APPLICANT: FOLKWAN, MOSES J.; KATO, KOICHI
TITLE OF INVENTION: ACID-RESISTANT FGF COMPOSITION AND METHOD
FOR TREATING ULCERAIING DISEASES OF THE GASTROINTESTINAL TRACT
                                                                                        399 AATTGGTTTGTTGGCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          399 AATTGTTGTTGCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 AATTGGTTTGTTGGCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.2%; Score 186; DB 6; Length 454; 99.3%; Pred. No. 2.2e-87; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.0%; Score 172; DB 6; Length 197; 100.0%; Pred. No. 4.4e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FIDDES, JOHN C.; ABRAHAM, JUDITH A. TITLE OF INVENTION: METHODS OF PRODUCING RECOMBINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/382,263 FILING DATE: 20-JUL-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/417,022 FILING DATE: 05-APR-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 234,966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 809,163
FILING DATE: 16-DEC-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 775,521
FILING DATE: 12-SEP-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-AUG-1988
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.38
Matches 286; Conservative
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                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 21
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                                                                                                                                                                                                                              ,Patent No. 5175147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5514566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 454
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5175147-1
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US-09-030-613-14

Gaps

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122 ATGGCTGAAGGGGAAATCACCACCTT 147
                                     39 ATGGCTGAAGGGGAAATCACCACCTT 64
26; Conservative
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                                                                                                                                                             5514566-1
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                                                                                    282 AIGGACACCGACGGCTITIAIACGGCTCACAGACACCAAAATGAGGAATGTITGTTCCTG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT
TITLE OF INVENTION: AND METHODS FOR IDENTIFYING AND USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Chemically synthesized sequence for human acidic OTHER INFORMATION: Fibroblast Growth Factor (155 amino acids) using OTHER INFORMATION: preferred codons for E. coli
           ch 12.1%; Score 77; DB 3; Length 454; 1 Similarity 100.0%; Pred. Mo. 1.99-30; 77; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.1%; Score 77; DB 4; Length 454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.9e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. ...
Warches 77; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 200124,40204
CURRENT APPLICATION NUMBER: US/09/451,905
CURRENT FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: CYCENG.008A
CURRENT APPLICATION NUMBER: US/09/929,945
CURRENT FILING DATE: 2001.08-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                 . Sequence 14, Application US/09451905
; Patent No. 6306613
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Robert Z. Florkiewicz
APPLICANT: Andrew Baird
APPLICANT: Dale E. Warnock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/09929945
; Patent No. 6642026
                                                                                                                                                                                            306 GAAAGGCTGGAGGAGA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Slavchenko, Iryna Yu. APPLICANT: Vozianov, Oleksandr
                                                                                                                                                                     342 GAAAGGCTGGAGGAGAA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Stegmann, Thomas
APPLICANT: Kordyum, Vitaliy A.
APPLICANT: Chernykh, Svitlana I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 GAAAGGCTGGAGGAGAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 GAAAGGCTGGAGGAGAA 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (122)...(590)
US-09-929-945-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapien
        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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LENGTH: 630
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                                                Matches
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Query Match 4.1%; Score 26; DB 4; Length 630; Best Local Similarity 100.0%; Pred. No. 0.00086;

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0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Seddon Dr., Andrew P.
APPLICANT: Bohlen Dr., Peter
APPLICANT: Gluzman Dr., Yakov
TITLE OF INVENTION: Chimeric Fibroblast Growth Factors
Patent No. 5514566
; APPLICANT: FIDDES, JOHN C.; ABRAHAM, JUDITH A.
; TITLE OF INVENTION: METHODS OF PRODUCING RECOMBINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity 100.0%; Pred. No. 0.00
24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES; 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
                                                                                                                                         APPLICATION NUMBER: US/08/417,022
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,219-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 CAGCTGCTGAGCCATGGCTGAAGG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 CAGCTGCTGAGCCATGGCTGAAGG 32
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FILING DATE: 23-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/023,757
FILING DATE: 26-FEB-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 8, Application US/08023757; Patent No. 5302702
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                                                                                                                                                                                                             APPLICATION NUMBER: 809,163
FILING DATE: 16-DEC-1985
                                                                                                                                                                                                                                                            APPLICATION NUMBER: 775,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-321-2756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                FILING DATE: 12-SEP-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 710-474-4059
INFORMATION FOR SEQ ID NO:
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                                                                                          NUMBER OF SEQUENCES: 21
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PRIOR APPLICATION DATA:
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STRANDEDNESS: single
                                                                   FIBROBLASTS GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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ZIP: 06904-0060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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Matches

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; Patent No. 5387673
; GENERAL INFORMATION:
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                                                                                                                3.6%; Score 23; DB 1; Length 44;
                                                                                                                                                       0; Indels
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100.0%; Pred. No. 0.028;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Seddon Dr., Andrew P.
APPLICANT: Bohlen Dr., Peter
APPLICANT: Gluzman Dr., Yakov
TITLE OF INVENTION: Chimeric Fibroblast Growth Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                100.0%; Pred. No. 0.028;
tive 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: American Cyanamid Company
STREET: 1937 West Main Street, P. O. Box 60
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-321-2756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/177,502
FILING DATE: 0S-CAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 26-FEB-1993
APPLICATION NUMBER: US/07/615,202
                                                                                                                                                                                       39 ATGGCTGAAGGGGAAATCACCAC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/023,757
                                                                                                                                                                                                                            9 ATGGCTGAAGGGGAAATCACCAC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 ATGGCTGAAGGGGAAATCACCAC 61
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                                                                                                                                                                                                                                                                                                                      ; Sequence 8, Application US/08177502
; Patent No. 5371206
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Tsevdos Dr., Estelle J. REGISTRATION NUMBER: 31,145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/08054650A
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 203-321-2971
TELEX: 710-474-4059
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                   23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100. Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                              Best Local Similarity
                                                         ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06904-0060
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stamford,
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                    ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                 RESULT 13
US-08-177-502-8
                                                                         US-08-023-757-8
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                                                                                                                  Query Match
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APPLICANT: Seddon, Andrew P
APPLICANT: Seddon, Andrew P
TILLE OF INVENTION: Active Fragments of Fibroblast Growth
TITLE OF INVENTION: Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.6%; Score 23; DB 1; Length 44;
100.0%; Pred. No. 0.028;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dr. Estelle J. Tsevdos
STREET: 1937 West Main Street, P.O. Box 60
                                                                                                                                                                 STREET: 163 Delaware Avenue, Suite 212 CITY: Delmar STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/054,650A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 06504-006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 31309-01
                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/383,621
FILING DATE: 06-FEB-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 ATGCTGAAGGGGAAATCACCAC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 ATGGCTGAAGGGGAAATCACCAC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Daley, Michael J.
APPLICANT: Buckwalter, Brian L.
APPLICANT: Cady, Susan M.
APPLICANT: Shieh, Hong-Ming
APPLICANT: Solien, Peter
APPLICANT: Seddon, Andrew P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Sequence 11, Application US/08383621
. Patent No. 5951972
                                                                                                                                             ADDRESSEE: Anne M. Rosenblum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (518)475-0611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Tsevdos, Estelle J. REGISTRATION NUMBER: 31145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-APR-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 11
                                                                                                NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Stamford
STATE: Connect:
                                                                                                                                                                                                                                      USA
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ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3, Application US/09902460; Publication No. US20030040042A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FIDDES, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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6501.952 Million cell updates/sec
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2: /cgm2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgm2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
4: /cgm2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
5: /cgm2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgm2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgm2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
9: /cgm2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgm2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
10: /cgm2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                August 24, 2004, 21:00:28 ; Search time 482 Seconds
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/cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq2:*
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/cgm2_6/ptodata/1/pubpma/US10B_PUBCOMB.seq:*
/cgm2_6/ptodata/1/pubpma/US10C_PUBCOMB.seq:*
/cgm2_6/ptodata/1/pubpma/US10C_PUBCOMB.seq:*
/cgm2_6/ptodata/1/pubpma/US10_NEW_PUB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.6%; Score 23; DB 2; Length 44; Best Local Similarity 100.0%; Pred. No. 0.028; Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3228839 seqs, 2456066551 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM nucleic - nucleic search, using sw model
NAME: Tsevdos, Estelle J.
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,278-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-321-2756
TELEFAX: 203-321-2756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: August 24, 2004, 23:07:01 Job time : 87 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_NA:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 ATGGCTGAAGGGGAAATCACCAC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 ATGGCTGAAGGGGAAATCACCAC 31
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                                                                                                                                                                                     11:
                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                      TELEX: 203-710-474-4059
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-022-554A-3
                                                                                                                                                                                                                                   LENGTH: 44 base pairs
                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OLIGO NUC
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US-08-383-621-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
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18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBGOMB.seq:*

APPLICATION NUMBER: US 07/766,142

FILING DATE: 25-SEP-1991 ATTORNEY/AGENT INFORMATION:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	ult. No.	Score	Query Match	Query Match Length	DB	qI	, to
1							nescribtion
	н	434	68.0	63	10	-09-902-460	Sequence 3, Appli
	7	434	68.0	4087	14	US-10-044-090-225	225
	m	418	65.5	490	15	US-10-388-410-8	80
	4	418				US-10-641-643-1390	
	S)	408	63.9		6	US-09-929-918-3	Sequence 3, Appli
	9	408		468		US-09-929-945-3	•
	7	408		468		US-10-280-864-3	
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υ	σ	195	30.6			US-09-864-761-13391	. ני
U	10	187	29.3	187	_	0	
	11	147	23.0		16	US-10-116-275-235	Sections 225
	12	135	21.2	m	17	US-09-968-007A-133	1 2 4
	13	135	21.2	3658	12	US-09-968-007A-440	440,
	14	56	4.1	65	10	US-09-908-975-28515	285
	15	26	4.1	630	0		Semience 1 Annli
	16	56	4.1	630	6	US-09-929-945-1	
	17	26	4.1	630	15	US-10-280-864-1	` -
	18	26	4.1	630	17	US-10-649-480-1	•
	19	26	4.1	990	σ	US-09-929-918-10	i
	20	22	3.4	29	70	US-09-847-936B-13	
υ	21	21	3.3	28	10	-09-847-936B-1	Segmence 12 Appl
	22	21	3.3	630			
	23	21	3.3	630	σ	US-09-929-918-6	, v
	24	21	3.3	630		US-09-929-945-4	, 4
	25	21		630		US-09-929-945-6	٠ د
	56	21	3.3	630	15	US-10-280-864-4	. 4
	27	21	3.3	630	15	US-10-280-864-6	9
•	28	21	3.3	630	17	US-10-649-480-4	4
	53	21		630	11	US-10-649-480-6	9
	30	70	3.1	20	10	US-09-981-803-19	19,
	37	20		20	15	US-10-104-025-1	H
	32	20	3.1	637	13	US-10-027-632-188645	188
	£ .	70	3.1	637	13	US-10-027-632-188646	
U .	34	20	3.1	637	16	4	
	ر د د	20	3.1	637	w	US-10-027-632-188646	18864
	919	13	3.0	581		US-09-864-761-9138	ტ
υ		19	3.0	1231	17	US-10-437-963-22726	227
		19	3.0	2121	7	US-10-437-963-64740	64740.
	39	13	3.0	2715		US-09-764-870-65	NO.
•	0	19	3.0	2715	15	US-10-125-540-65	. 65,
ט	4. T	6	3.0	4270	15	US-10-000-256A-84	84,
4	2	19	3.0	4715	13	-10-	473,
4	en :	13	3.0	5111	13	-10-342	182,
4	44	19			13	10-	182
Ω	ı,	19	0 M	2256646	17	US-10-470-565-1	ц,

TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH PACTOR ANALOG COUNTRY: USA ZIP: 94304-1018

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GENERAL INFORMATION:
APPLICANT: NAMA, HIROYUKI
APPLICANT: TAKHARSHI, HITOSHI
APPLICANT: TRAHARSHI, HITOSHI
TITLE OF INVENTION: METHOD FOR DIACNOSING SCHIZOPHRENIA USING OBJECTIVE INDICES
FILE REFERENCE: 235447USGOCONT
                                                                                                                                                                                                                                                                                                                                                                                                                                            73 TGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 GCGCCACAAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCC 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 GCAACGGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGGACAAGGGACA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 GCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 AGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGCTTTTATACGGCTCAC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 AGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCATTACAACACT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              780 AGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCATTACAACACCT 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 ATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGCCTCAAGAAGAATGGGAGCT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       840 ATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGTCTCAAGAAGAATGGGGAGCT 899
                                                                                                                                                                                                                                                                                   Length 4087:
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                                                                                                                                                                                         ; NAME/KEY: misc_feature
; OTHER INVENTATION: Incyte ID No. US20020137081A1 336376.2
US-10-044-090-225
                                                                                                                                                                                                                                                                        68.0%; Score 434; DB 14; Lv
100.0%; Pred. No. 3.4e-215;
tive 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/044,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/388,410
CURRENT FILING DATE: 2003-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/723,224
PRIOR FILING DATE. 2000-11-28
PRIOR APPLICATION NUMBER: JP 2000-061775
PRIOR FILING DATE. 2000-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/10388410
Publication No. US20030157548A1
                  CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                     Matches 434; Conservative
                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                       LENGTH: 4087
                                                                                 SEQ ID NO 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 490
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                                                                                                                              TYPE: DNA
                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 GCGCCACAAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 IGACCGAGAAGITITAAICIGCCICCAGGGAAITACAAGAAGCCCCAAACICCICCICTACIGIA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 GCAACGGGGGCCACTICCTGAGGATCCTTCCGGATGGCACAGTGGATGGGACAAGGGACA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 AGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAAGGAGAAGCCATTACAACACT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 ATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGGCTTCAAGAAGAAGAATGGGAGCT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 GCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAAATCACCACCTTCACAGCCC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 GGAGCGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGAGGTGTATATAA 304
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                                                                          SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 68.0%; Score 434; DB 10; L. Best Local Similarity 100.0%; Pred. No. 3.9e-215; Matches 434; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                            NAME: Lehnhardt, Susan K
REGISTRATION NUMBER: 33,943
REPERRUCE/DOCKET NUMBER: 21900-20089.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                APPLICATION NUMBER: US/09/902,460
FILING DATE: 09-Jul-2001
                                                                                                                                                                                                    APPLICATION NUMBER: 09/098,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Coding Sequence
                                                                                                                                                           CLASSIFICATION: <Unknown>
                               COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 225, Application US/10044090; Publication No. US20020137081A1; GENERAL INFORMATION:
                                                                                                                                                                                                                          FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 638 base pairs
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
               MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                           PRIOR APPLICATION DATA:
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MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
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Gaps

COMPUTER READABLE FORM

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29 CTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAGTTTAA 88
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Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 29 CTGCTGAGCCATGACTGAAATTCACCACCTTCACAGCCCTGACCAGAATTTAA 88			Qy 269 CCAGTACTTGGCCATGGACACGGGGCTTTTTATACGGCTCACAGACACCAAATGAGA 328	g-g :	RESULT 5 US-09-929-918-3	: Sequence 3, Application US/09929918 ; Patent No. US2002009678A1 · FENERD1. INTRODAMTION	,			FILE REFERENCE: PHAG CURRENT APPLICATION	; CURLENT FILING DATE: 2001-08-15 ; PRIOR APPLICATION UNDERS: 09/318,288 . DBIOD DITING DATE: 1000.01	; NUMBER OF SEQ ID NOS: 11 ; SOFTWARE: FastSEQ for Windows Version 4.0	SEQ ID N	; TYPE: DNA ; ORGANISM: Homo sapiens US-09-929-918-1	63.9%; Score 408;		2y 3.9 ATGGCTGAAGGGAAATCACCACCTTCACAGGGCGTGAAGTTTAATCTGCCTCCA 98	Db 1 ATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACGGAAGTTTAATCTGCCTCCA 60	QY 99 GGGAATTACAAGAGCCCAAACTCCTCTACTGTAGCAACGGGGGGCCACTTCCTGAGGATC 158	Db 61 GGGAATTACAAGAAGCCCAAACTCCTCTACTAGCAACGAGGCCACTTCCTGAGGATC 120	QY 159 CTTCCGGATGGCACAGTGGATGGGACAGGACGACGACCAGCACATTCAGCTGCAG 218	Db 121 CTTCCGGATGGCACAGTGGATGGACAAGAGGACGAGGAGGAGCAGCAGCACATTCAGCTGCAG 180	QY 219 CTCAGTGCGGAAAGCGTGGGGGGGGTGTATAAAAGAGTACCGAGACTGGCCAGTACTTG 278	Db 181 CTCAGTGCGGAAAGCGTGGGGGAGAGTATATAAAGAGTACCGAGACTGGCCAGTACTTG 240	OY 279 GCCATGGACACCGACGGCTTTTATACGGCTCACAACCAAATGAGGAATGTTTGTT
1 CTGCTGAGCCATGGAGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAA 89 TCTGCCTCCAGGGAATTACAAGAAGCCCAAACTTCCTTCTACTGTAGCAACGGGGGAAGTTTAA 61 TCTGCCTCCAGGGAATTACAAGAAGCCCAAACTTCCTCTTACTGTAGCAACGGGGGCCACTT 61	WY 149 COLORGANICOTTCCGGATGGCAGGGAGGAGGAGGCAGCACACACATT 208 121 CCTGAGGATCCTTCCGGATGGCAGGTGGATGGGACAGGAGGGACCACACACA	269	QY 329 AIGITIGITCCTGGAAAGGCTGGAGAAAACCATTACAACACTATATATCCAAGAAGCA 388 	Qy 389 TGCAGAGAAATTGGTTTGTTGGCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCT 446 	FUDITCE	Shand G. Standard C. Standard	TITLE OF IN	NUMBER OF SEQUENCES: 1508 CORRESPONDENCE ADDRESS:	ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 POPTER DRIVE			MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible OPPRATING SVETTEM: DATE OF THE OFFICE OF THE OFFICE OFFI	TARIL TARIN	FILING DATE: 14-Aug-2003	CLASSIFICATION: <unknown> PRIOR APPLICATION DATA: ADDITICATION NIMBED: Ithicacon.</unknown>	ATTOR	NAME: Zeller, Karen J. REGISTRATION NUMBER: 37	TELEC	TELEP! TELEF!	INFORMATIO SEQUE		; STRANDENESS: single ; TOPOLOGY: linear	; IMMEDIATE SOURCE: ; LIBRARY: GENBANK	; SEQUENCE DESCRIPTION: SEQ ID NO: 1390 :	Query Match Query Match 65.5%; Score 418; DB 17; Length 490; Best Local Similarity 100.0%; Pred. No. 8.4e-207;

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99 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGGCCCACTTCCTGAGGATC 158
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                                                                                399 AATIGGITITGITGGCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCT 446
                                                                                                         399 ANTIGGITIGITIGGCCTCAAGAAGAATGGGAGCTGCAAACGCGGTCCT 446
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                                                                                                                                                                                                                                                                                                                                APPLICANT: Chernykh, Svitland I.
APPLICANT: Slavchenko, Iryna Yu.
APPLICANT: Vozanov, Oleksandr V.
APPLICANT: Vozanov, Oleksandr V.
TITLE OF INVENTION: SIPER PRODUCTION OF RECOMBINANT ITILE OF INVENTION: FIBROBLAST GROWTH FACTOR 155
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APPLICANT: Chernykh, Svitlana I.
APPLICANT: Slavchenko, Iryna Yu.
APPLICANT: Vozianov, Oleksandr
TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. w..
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CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                               ; Sequence 3, Application US/09929945
; Patent No. US20020155532A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3, Application US/10280864; Publication No. US20030054492Al; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          APPLICANT: Stegmann, Thomas
APPLICANT: Kordyum, Vitaliy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: CVGENG.008A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0
Matches 408; Conservative
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                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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99 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGCCACTTCCTGAGGATC 158
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                                                                                          39 ATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCA
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63.9%; Score 408; DB 15; Length 468; 100.0%; Pred. No. 1.3e-201; Live 0; Mismatches 0; Indels
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0; Mismatches 0;
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PRIOR FILING DATE: 2003-03-27
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Publication No. US20040115769A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chernykh, Svitlana I. APPLICANT: Slavchenko, Iryna Yu. APPLICANT: Vozianov, Oleksandr
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                                              Matches 408; Conservative
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                          Best Local Similarity
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  Query Match
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NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3

TYPE: DNA ORGANISM: Homo sapiens

US-10-280-864-3

LENGIH: 468

PRIOR APPLICATION NUMBER: US/09/929,945 PRIOR FILING DATE: 2001-08-15

CURRENT FILING DATE: 2002-10-24

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; OTHER INFORMATION: MAP TO ACO10489.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
US-09-864-761-13391
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   ORGANISM: Homo sapiens
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                                                                                                 121 CTTCCGGATGGCACAGTGGATGGGACCAGGAGCGACCAGCACCAGTCAGCTGCAG 180
                                                                                                                                                                                                                   301 CTGGAAAGGCTGGAGGAGAACCATTACAACACCTATATATCAAGAAGAAGCATGCAGAGAAG 360
                                                            159 CTTCCGGATGGCACAGTGGGACAGGGACAGGAGCGACCAGCACCATTCAGCTGCAG 218
                                                                                                                                                                                                                                                                                                              339 CTGGAAAGGCTGCAGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGAAG 398
61 GGGAATTACAAGAAGCCCAAACTCCTCTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 120
                                                                                                                                                                                     219 CTCAGTGCGGAAAGCGTGGGGGAGGTGTATAAAAGAGTACCGAGACTGGCCAGTACTTG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399 ANTIGGITTGTTGGCCTCAAGAATGGGAGCTGCAAACGCGGTCCT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/23,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2001-01-03
PRIOR PAPLICATION NUMBER: PCT/US01/00667
PRIOR PAPLICATION NUMBER: PCT/US01/00667
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
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CURRENT APPLICATION NUMBER: US/09/864,761
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-09-21
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NUMBER OF SEQ ID NOS: 49117
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US-09-864-761-13391/c
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
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                                                                                                                                                                                                                                                                                                                                                                 212 TGACGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTA 153
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        Length 580;
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                                                                                0; Indels
1 30.6%; Score 195; DB 9; L
Similarity 100.0%; Pred. No. 8.1e-91;
95; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR PLING DATE: 2001-01-30
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PRIOR PELING DATE: 2001-01-30
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CURRENT APPLICATION NUMBER: US/09/864,761
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PRIOR APPLICATION NUMBER: US 60/207,456
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TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Usining
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                                                                                                                                                     FILE REFERENCE: 689290-71
CURRENT APPLICATION NUMBER: US/09/968,007A
CURRENT FILING DATE: 2001-10-02
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PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR PELING DATE: 2000-10-02
PRIOR PELING DATE: 2000-10-02
PRIOR PELING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,295
PRIOR PILING DATE: 2000-10-02
PRIOR PLING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
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PRIOR FILING DATE: 2000-10-02
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; Sequence 440, Application US/09968007A
; Publication No. US20040115625A1
        Publication No. US20040115625A1
                                                                                                                                 TITLE OF INVENTION: Gene Sets
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                                                    APPLICANT: Ebner, Reinhard
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods
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                                                                                                                                                                           INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
INFORMATION: EST HUMAN HIT: A51590078.1, EVALUE 1.00e-101
INFORMATIONS: WISSPROT HIT: P05230, EVALUE 6.00e-29
INFORMATION: NT HIT: GII11416219, EVALUE 1.00e-101
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                                                                                                                                                                                                                                                                                                                                      29.3%; Score 187; DB 9; Length 187;
                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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CURRENT APPLICATION WOMER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
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                                                                                                                                                     OTHER INFORMATION: MAP TO AC010489.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 235, Application US/10116275; Publication No. US20030211476A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: 0'Mahony, Daniel J. APPLICANT: Brayden, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin version 3.1
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APPLICANT: Lambkin, Imelda
APPLICANT: Higgins, Lisa
                                                                       TYPE: DNA ORGANISM: Homo sapiens
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                        ; SEQ ID NO 29943
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US-10-116-275-235
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                                                 LENGTH: 187
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APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLECTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND
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                                                                             312 CAGACACCAAATGAGGAATGTTTGTTCCTGGAAGGCTGGAGGAGAACCATTACAACACC 371
                                                                                                         304 CAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAACCATTACAACACC 363
                                                                                                                                                                               372 TATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGCCTCAAGAAGAATGGGAGC 431
                                                                                                                                                                                                             364 TATATATCCAAGAAGCATGCAGGAGAAGAATTGGTTTGTTGGCCTCAAGAAGAATGGGAGC 423
                           0; Gaps
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APPLICANT: Chernykh, Svitlana I.
APPLICANT: Slavchenko, Iryna Yu.
APPLICANT: Vozianov, Oleksandr
TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
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  100.0%; Pred. No. 1.1e-59; tive 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/908,975
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CURRENT APPLICATION NUMBER: US/09/929,918
CURRENT FILING DATE: 2001-08-15
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PRIOR FILING DATE: 2001-05-02
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; Publication No. US20030165843A1
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PRIOR FILING DATE: 1999-05-25
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; Patent No. US20020090678A1
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                                                                                                                                                                                                                                                                                   432 TGCAAACGCGGTCCT 446
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                         135; Conservative
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US-09-908-975-28515
Best Local Similarity
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Query Match 4.1%; Score 26; DB 9; Length 630; Best Local Similarity 100.0%; Pred. No. 0.0065; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                        Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                            GenCore version 5.1.6
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                                                                                            122 ATGCTGAAGGGAAATCACCACCTT 147
                                                                39 ATGGCTGAAGGGGAAATCACCACCTT 64
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Job time : 485 secs
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Maximum DB seq length: 200000000
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OTHER INFORMATION: codons which are used in highly expressed proteins from E.

LOCATION: (122) ... (590)

NAME/KEY: CDS US-09-929-918-1

and is derived by analysis of the total score distribution.

SUMMARIES

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

	1.x	0094 Our-	OURT	567 FE	362U 019	9744	N023	/526 SURT	586G	-60-	2.r 7981	x.7	x. 7	\$024 \$D0-	딕	9586	tal OR	318	MA .	w .	r1 111-		du x.	7.9H 4.76	686 QY		or 7.50 96	992 QY	62 Db		38 QY	916 Db	2.2 QY	qa	, O _Y	qq	1999 Ov	ı	qa	70	qū				L; RES BIS LOC LOC DEF		
AI590078 tm58c01.x		BI598390 603250094 BM809005 AGENCOIDE	BQ067949 AGENCOURT	BX444567 BX44456	CD701495 EST18019	BG706412 602669744	BF956865 RC1-NN023	BU840197 AGENCO		m	AAU15793 ze30a12.r BI598882 60324798	A1864448 w153c07.x	AI083919 q£26c07	BM995210 UI-H-ED0	H23109 ym51f12.rl	AI077609 ov26d02.	R58184 F9465 Fet	BI550213 6031923 R14113 VF69e06	BF442355 259038 MA	AA594274 n190g01.	K54255 YG/4106.rl AW207545 UI-H-BI1-	BQ006006 UI-H-EI	AI359575 qy32c08.	GG568464 OST195476		CG496943 OST37278 CG605210 OST28165	·	CG620633 OST3179	BY302462 BY30246	BY234021 BY23402	BY230638 BY23063 BY235986 BY23598	2 12 1	4										tebrata; Euteleostomi	Chordata, Craniata, Vertebrata, Euteleostomi, Primates; Catarrhini, Hominidae, Homo.	tebrata; Euteleostomi. Ominidae; Homo. noicgap. ute of Neurological	tebrata; Euteleostomi, ominidae; Homo. ncicgap. ute of Neurological	tebrata; Euteleostomi, ominidae; Homo. ncicgap. ute of Neurological atomy Project
QI	A1590078	B1598390 BM809005	BQ067949	BX444567 RIB69731	CD701495	BG706412	BF956865 BT753845	BU840197	BX488304	BU627243	BI598882	AI864448	AI083919 RF958824	4 4	H23109	AI077609	R58184	B1550213 R14113	BF442355	4A594274 R54255	AW207545	BQ006006	A1359575 BX501193	CG568464	CG558760	CG605210	BY349996	CG620633 BY141229	BY302462	BY234021	BY230638 BY235986	CG613113 BY237122		ALIGNMENTS			534 bp mRNA linear EST 21-APR-1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162304	EPARIN-BINDING GROWTH					ordata; Craniata; Ver	ordata; Craniata; Ver imates; Catarrhini; H	ordata, Craniata, Ver imates, Catarrhini, H. www.ncbi.nlm.nih.gov/,	Homo Saptens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 534) NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index	Homo Saptens Buckaryota; Metazoa; Chordata; Craniata; Ver Mammalia; Butheria; Primates; Catarrhini; H 1 (bases 1 to 534) NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/; Nozlonal Cancer Institute / National Institu Disorders and Stroke, Brain Tumor Genome An. (CGAP/BYGAP), Tumor Gene Index Unpublished (1998)
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Match	68.0	68.0	68.0	50.3	49.7	46.4	45.3	43.7	43.4	32.4	29.5	23.0	22.6	17.7	17.4	15.8	12.7	11.8	11.6	11.3	11.3	11.3	11.0	9.6	6.0	2.5	9.5	9.6	9.2	6.0	, o	9.5				1		_ =	078		sapiens (human)	Sanjen	sapiens Yota, M Jia: En	Homo sapiens Eukaryota, Metazoa; Mammalia, Eutheria; 1 (bases 1 to 534)	sapien: Yota; h lia; El ases 1 INDS-C(sapiens rota; h lia; Bl ases 1 INDS-CC nal Car ders al	Homo sapiens Eukaryota, Metazoe Bukaryota, Metazoe Mammalia; Eutheria NcI/NINDS-CGAP htt Notional Cancer Ir Disorders and Strc (CGAP/BTGAP), Thm Unpublished (1998)
- 1	434	434	434	321											111																	59				, C C L	tm58c(Similar to (HUMAN);	A1590078				Eukary Mammal	Eukary Mamma]	Eukary Mammal Mammal 1 (ba NCI/NI Natior	Eukary Mamma] 1 (be NCI/NI Nation Disord (CGAP/	nomo s Eukary Mammal 1 (bs NCI/NI Nation Disord (CGAP/ Unpubl
No. S	0 0	ım	4° u	n 49	7	no o	10	11	12		15		C 18		20	c 22	23	25	26			30		E :	ы ы 4, г.	36	37	o 6.	04,	41	43	4 4 5 4			FESITA 1	A1590078/c	DEFINITION		ACCESSION	KEYWORDS	SOURCE	ORGANISM	ORGANISM	ORGANISM REFERENCE AITHLOBG	ORGANISM REFERENCE AUTHORS TITLE	ORGANISM REFERENCE AUTHORS TITLE	ORGANISM REFERENCE AUTHORS TITLE JOURNAL

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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCT-CGRP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 736 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                             T 3'I; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 GCGCCACAAAGCAGCAGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 TGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAAGTCCTCTACTGTA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     470 TGACCGAGAAGITTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 GCAACGGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGGACAAGGGACA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 GGAGCGACCAGCACATTCAGCTGCAGCTCAGTGCCGAAAGCGTGGGGGAGGTGTATATAA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 GGAGCGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGAGCTGTATATAA 291
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603250094F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5302030 5'',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 AGAGTACCGAGACTGCCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTCC 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.0%; Score 434; DB 9; Length 534; 100.0%; Pred. No. 2.2e-211; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                   /tissue_type="anaplastic oligodendroglioma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                             High quality sequence stop: 455.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                /clone="IMAGE:2162304"
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                                                                                                                                                                                                                                                                               /db xref="taxon:9606"
                                                                                                                                     Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
                                                                                                                                                                                                                                                         /mol_type="mRNA"
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EST.
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URCE
ORGANISM
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598390
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AGENCOURT_6617747 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5734445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 GCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCC 216
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  constructed by C. Gruber (Invitrogen). Research Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="organ: brain; Vector: pCMV-SPORT6; Site_1: ECORV (destroyed): Site_2: Not1: RNA source male hippocampus,
                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation (Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                     National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 434; DB 12; Length 1014;
Pred. No. 2.5e-211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC 124"
                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 637.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:5734445"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tracking code 012."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
                                                                                       BM809005.1 GI:19125828
                                                                                                                                                                                                                                        l (bases 1 to 1014)
                                                                                                                                      Homo sapiens (human)
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                                          mRNA sequence.
                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 434; Conservative
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                                                                                                                                                              Homo sapiens
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             DEFINITION
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                                                                                                                                                                                                                                                           AUTHORS
TITLE
                                                                                                            KEYWORDS
SOURCE
                                                                                                                                                                                                                                        REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 GCGCCACAAGCAGCAGCTGCTGAGGCTGAAGGGGAAATCACCACCTTCACAGCCC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 IGACCGAGAAGITITAAICIGCCICCAGGGAAITACAAGAAGCCCAAACICCICTACIGIA 132
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                                                                                                                                                                                              Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (MHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 GCAACGGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGGACAAGGGACA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 GGAGCGACCAGCACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGAGGTGTATATAA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 AGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGGCTTTTATACGGCTCAC 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insert size 2.3 kb and normalized to ROT 5. This is a
                                                                                               National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (groga); Oligo-dT primed using primer 5'-THTFITHTHTHTHTHNN-3', size-selected for average
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/note="Organ: brain; Vector: pBluescriptR (modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.0%; Score 434; DB 12; Length 821;
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High quality sequence stop: 777.
Location/Qualifiers
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                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                               1 (bases 1 to 821)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:5302030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab host="DH10B
                                                                                                                                                                                                                                                                                                                                                                    http://image.llnl.gov
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Qy 433 GCAAACGCGGTCCT 446 Db 535 GCAAACGCGGTCCT 548 RESULT 5 BX444567 LOCUS BX444567 Home sapiens ADULT BRAIN Home sapiens CDNA clone ACCESSION BX444567 Home sapiens ADULT BRAIN Home sapiens CDNA clone ACCESSION BX444567 Home sapiens ADULT BRAIN Home sapiens cDNA clone ACCESSION BX444567 GT GT:30780253 KEYWORDS EST. SQURCE Home sapiens (human) CRANTSM Home sapiens (human)	Eukaryort Mammalia 1 1, W.B., Ini, W.B., Ini, W.B., Contact: Genoscope Genoscope BP 191 97 Email: ss Invitrogy More info More		Qy 73 TGACCGAGAGTTTAATCTCCTCCAGGAATTACAAGAAGCCCAAACTCCTTACTGTA 132 Db 202 TGACCGAGAAGTTTAATCTCCTCCAGGAATTACAAGAAGCCCAAACTCCTCTACTGTA 261 Qy 133 GCAACGGGGCCACTTCCTCAGGAATCTCCCGATGCCAACTGGAACGCACA 192 db 262 GCAACGGGGCCACTTCCTCAGGATCCTTCCGGATGCGAAGCGCACA 192 dcAACGGGGGCCACTTCCTCAGGATCCTTCCGGATGCGAAGCGCACAGGGGACA 193 dcAACGGGGGCCACTTCCTCAGGATCCTTCCGGATGCGAAGCGGACATTATAA 252 db 262 GCAACGGGGCCACTTCAGCAGCTCAGTGCGAAGCGTGGGGGGGTGTATATAA 252 db 332 GGAGCGACCAGCACTTCAGCAGCTCAGTGCGGAAGCGTGGGGGGTGTATATAA 381 Qy 253 AGAGTACCGAGCTGCCAGTTCAGGCCATGGACACGGGGGGGTGTTTATAACGGCTCAC 41 dc 332 AGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACGGGGGGGTTTTATACACACCC 41 dy 333 AGACACCAAATGGGAATGCTTGGCAAGGCTGGACGAGAACCTTTACAACACCT 372 db 442 AGACACCAAATGAGAATGTTTGTTCCTGGAAAGGCTGGAGGAACCATTACAACACT 372 dy 373 ATATATCCAAATGAGAAATGTTTGTTCCTGGAAAGGCTGGAGGAACCATTACAACACT 501 dy 373 ATATATCCAAATGAGAAAGGTTTGTTCGTTGGCTCAAAGGAGAACCATTACAACACT 501
Σ . Σ		10.7-3.5 kb. 10.7-3.5 kb. 10.1N (Invitrogen) this is a NII (Invitrogen) this is a NII (Best Local Similarity 100.0%; Matches 434; Conservative (175 TGACCGAGAAGTITAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTA 234 133 GCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGA

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EST18019 human nasopharynx Homo sapiens cDNA, mRNA sequence.
                                                                                                                  CD701495.1 GI:32232125
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73 TGACCGAGAAGITITAAICTGCCTCCAGGGAAITACAAGAAGCCCAAACTCCICTACTGIA 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (phage-resistant)"
/clone lib="NHH MGC_90"
/note="Organ: liver; Vector: pCMV-SPORTS, Site 1: Not!;
Site 2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 GCGCCACAAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCC 113
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                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                               B1869731 832 bp mRNA linear EST 11-OCT-20 603393620F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5403677 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Plate: LiAMA12029 row: g column: 06
High quality sequence stop: 829.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="adenocarcinoma, cell line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.3%; Score 321; DB 12; L
Best Local Similarity 100.0%; Pred. No. 2.6e-153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                       433 GCAAACGCGGTCCT 446
                                                                                       562 GCAAACGCGGTCCT 575
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                           1 (bases 1 to 522)
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
library from southern Chinese"
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1 (bases 1 to 714)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                Transcriptional Gene Expression Profile of Human Nasopharynx Unpublished (2003)
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                                                                                                                                                                                                                                         Cancer Center
Sun Yar-sen University
651 DongFeng Road East, GuangZhou 510060, China
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     Email: yxzeng@gzsums.edu.cn.
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                                                                                                                                                                                                                                                                                                                   Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Homo sapiens (human)
                                                                                                                                                                                                                    Contact: YiXin Zeng
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TITLE
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linear EST 25-JUN-2003

mRNA

522 bp

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J. TITLE Shotgun sequencing of the human transcriptome with ORP expressed sequence tags JOURNAL PROC. MALL. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) REDLINE SOUSSES DOORAGE: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Reazil Tel: +55-11-2704922 Fax: +55-11-27049233- Location/Qualifiers Location/Qualifier	QV 21S GCAGCTCAGGAAAGCGTGAAATAAAAAGAGTACCAGGA 274 Qy 21S GCAGCTCAGAAAGCGTGAAAGAGTAATAAAAAGAGTACCAGGACTGACCAGTA 274 Qy 21S GCAGCTCAGTGCAAAGCGTGAAGGGACAAGAGGACCACACACA	104 GCAGCTCAGTGCGGAAAGCGTGGGGGAGGTTATAGAGGTGCGGGAGATGCTGGCCAGTTA	RESULT 10 B1753845 LOCUS B1753845 LOCUS B1753845 LOCUS B1753845 ACCESION B1753845 RENEWORDS EST. SOURCE B1753845 HOMO Sapiens CNGANISM REFERENCE Librage Authoro. Authoro. Authoro. Authoro. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D. COMMENT Contact: Robert Strausberg, Ph.D. Email: Capabs=remail.uih.gov Tissue Procurement: Mixlos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki TOSHLyuki and Patero Carninnic (RIKEN) CDNA Library Arrayed By: The ILM.A.G.E. Consortium (LIML) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: DNA Sequence Stop: To. Clone distribution: MGC clone distribution information can be http://image.libr.gov Plate: LiAM10670 row: h column: 11 High quality sequence stop: 710. High quality sequence stop: 710. Righ quality sequence stop: 710. Ada. hoge="ManNa" (Ada. refe="Laxon:960" (Ada. refe" (Ada. refe" (Ada. refe = "Laxon:960" (Ada. ref	210 210 160 270 220	Db 330 TCAGTGGGGAAAGGTGTATATAAAAGATAACGAGACTGGCAATACTGA 389 Qy 280 CCATGGACACGACGGGCTTTTATACGCCTCACACACACAC	RESULT 9 BP95665 LOCUS L

COMMENT SPEATURES SOUTCE	Contact: Robert Strausberg, Ph.D. Email: capbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Incyck Genomics, Inc. Clone distribution: MGC clone distribution information can be there,://image.lln/gov Round Library Arrayed by: The I.M.A.G.E. Consortium/LIML at: Location/Oualifiers Location/Oualifiers 1. 878 Abrea = "HAMDES Proper Proper
Query Match Best Local Matches 28	Match 44.2%; Score 282; DB 12; Length 878; social Similarity 100.0%; Pred. No. 2.8e-133; 282; Conservative o: Mismatches o: Indials o: Cane
Qy Dp	GCCACTICCTGAGGATCCTTCCGGATGGCACACTGGAT 17
Db Cy	
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RESULT 11 BUB40197 LOCUS DEFINITION DEFINITION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT	BUB40197 AGENCOUTE 8964623 NIH_MGC_42 Homo sapiens CDNA clone IMAGE:6379201 5', maNA sequence. BUB40197 I GI:24024592 EST. Homo sapiens (human) Homo sapiens

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Once Togan: pancress; Vector: pOTB7; Site 1: XhoI; Site 2: ECORI; CDNA made by oligo-dT priming.

Site 2: ECORI; CDNA made by oligo-dT priming.

Directionally cloned into ECORI/XhoI sites using the following 5: adaptor: GGCACCAG(G). Size-selected >500pp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Supersoribt II RT (Life Technologies).

Note: this is a NIH_MGC Library. | "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 GGCACAGTGGATGGGACAAGGGACAGGACCACCACCATTCAGCTGCAGCTCAGTGCG 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKFZp686G16269_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686G16269 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NHF_MGC_42"
                                                                                                                                                                                                                                                                                                                                                           43.7%; Score 279; DB 13; Length 611; 100.0%; Pred. No. 9e-132;
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This is the 5' sequence of the clone insert
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Matches 279; Conservative
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http://image.llnl.gov Plate: LLCM2565 row: n column: 02 High quality sequence stop: 610. Location/Qualifiers

1. 611 /organism≈"Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:6379201"

source

FEATURES

/mol_type="mRNA"

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/note="Organ: Bone; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1; modified polylinker; Site 1: EcoR 1; Site 2: Not 1; to a coNA library containing the following tissue(s): Enchondroma cell line (2 cell lines). The library was constructed according to Bonaldo, Lennon and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear EST 23-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 TGACCGAGAAGITIAATCIGCCICCAGGGAATTACAAGAAGCCCAAACTCCICTACIGIA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 GCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGGACAAGGGACA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 GGAGCGACCAGCACATTCAGCTGCAGCTCCGGAAAGCGTGGGGGAGGTGTATAA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 750)
                                                                                                                                                                                                                                                                                                                                     13 GCGCCACAAGCAGCAGCTGCTGAGCCATGAAGGGGAAATCACCACCTTCACAGCCC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BU627243
U.-H-FG0-bct-n-05-0-UI.S1 NCI_CGAP_EN1_2 Homo sapiens CDNA clone
UI-H-FG0-bct-n-05-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                        /note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                  43.4%; Score 277; DB 13; Length 420; 100.0%; Pred. No. 8.9e-131;
                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from Dr. M. Bento Soares, bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Enchondroma cell line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 AGAGTACCGAGACTGGCCAGTACTTGGCCATGGACAC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 AGAGTACCGAGACTGGCCAGTACTTGGCCATGGACAC 420
                                                                                                                                         /clone_lib="686 (synonym: hlcc3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="UI-H-FG0-bct-n-05-0-UI"
                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: James Martin
           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _xref="taxon:9606"
                                                                            /clone="DKFZp686G16269"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                 /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
                                                                                                 /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13 FORWARD POLYA=Yes.
                                                                                                                                                                                         cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BU627243.1 GI:23293457
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                                                                                                                                                                                                                                                                                                      277; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
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                                                                                                                                                                                                                                                                                 Best Local Similarity
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source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
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                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
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EST 29-NOV-1996
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Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Nor I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dr)18 tail. The sequence tag for this library is CCGTCAGTC. The coll lines was provided by Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   675 GAGGTGTATATAAAAAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGACGGCTT 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 TTATACGGCTCACAGACACCAAATGAGGAATGTTTGTTCCTGGAAAGGCTGGAGGAGAAAC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 CATTACAACACCTATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGGCCTCAAG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 3013 Std Error: 0.00
                                                                                                                                                                                                                        James Martin from University of Iowa.

TAG TISSUE-Enchondroma cell line (Mix of EN1 and EN2)
TAG_LIB=UI-H-FG0
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                          Length 750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ö
                                                                                                                                                                                                                                                                                                                                                                                          32.4%; Score 207; DB 13; 100.0%; Pred. No. 8.9e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. wc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 AAGAATGGGAGCTGCAAACGCGGTCCT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           495 AAGAATGGGAGCTGCAAACGCGGTCCT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 372.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:360478"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                    TAG_SEQ=CGGTCACTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA015793.1 GI:1476960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 460)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .460
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                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
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double-stranded cDNA was size selected, ligated to ECC RI adapters (Pharmacia), digested with Not I and cloned into the Not I and ECC RI sites of a modified ppTT3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A) + RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. " /clone_lib="Soares retina N2b4HR"
/note="Organ: eye; Vector: pT/TID (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand colf, was primed with a Not I - oligo(dI) primer [5] IGITACCAATCIGAAGIGGGGGGGGCGCGTITITITITITITITITIT 3'],

ORIGIN

ö 73 TGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTA 132 183 TCACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTCCTCTACTGTA 242 133 GCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGGACAAGGGACA 192 72 0; Gaps Query Match 32.1%; Score 205; DB 9; Length 460; Best Local Similarity 100.0%; Pred. No. 8.6e-94; Matches 205; Conservative 0; Mismatches 0; Indels 193 GGAGCGACCAGCACATTCAGCTGCA 217 303 GGAGCGACCAGCATTCAGCTGCA 327 à g ઠે g ò 셤

RESULT 15 BI598882

BIS98882 570 bp mRNA linear EST 07-SEP-2001 603247981F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:5299508 5', Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. BIS98882.1 GI:15491821 Homo sapiens (human) mRNA sequence. BI598882 Homo sapiens DEFINITION ORGANISM ACCESSION KEYWORDS VERSION SOURCE

1 (bases 1 to 570)
NIH-MGC http://mgc.nci.nih.gov/. Unpublished (1999) REFERENCE AUTHORS

Email: cgapbs-remail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIEM) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Incyte Genomics, Inc. National Institutes of Health, Mammalian Gene Collection (MGC) Contact: Robert Strausberg, Ph.D. TITLE COMMENT

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Plate: LLAM11758 row: b column: 21 High quality sequence stop: 570. Location/Qualifiers

source FEATURES

1. .570

'tissue_type="hypothalamus" /organism="Homo sapiens" /clone="IMAGE:5299508" /db_xref="taxon:9606" /mol_type="mRNA" /lab host="DH10B"

insert size 2.3 kb and normalized to ROT 5. This is a Vector: pBluescriptR (modified /clone_lib="NIH_MGC_96" /note="Organ: brain; Vec

primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

Query Match

124 GCGCCACAAGCAGCAGCTGCTGAAGGCTGAAGGGGAAATCACCACCTTCACAGCCC 183 13 GCGCCACAAGCAGCAGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCCC 72 Best Local Similarity 100.0 Matches 188; Conservative à 윱 à

0; Gaps

0; Indels

0; Mismatches

29.5%; Score 188; DB 12; Length 570; 100.0%; Pred. No. 4.8e-85;

133 GCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGGACAAGGGACA 192 임 ò

193 GGAGCGAC 200 ð

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304 GGAGCGAC 311

Search completed: August 24, 2004, 23:05:24 Job time : 2849 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

August 14, 2003, 10:21:43 ; Search time 41 Seconds	(without alignments)	Can behalves [at conting can you
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1 ABGEITTFTALTEKFNIPPG.......PRTHYGQKAILFLPLPVSSD 154 US-10-022-554A-4 Title: Perfect score: Sequence:

1107863 meqm, 158726573 remidues Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum March Ot Maximum March 1004 Listing first 45 summaries Minimum DB meg length: 0 Maximum DB meg length: 2000000000

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, at derived by analysis of the total score distribution;

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		Description	endoth	Human beta-endothe	Human beta-endothe	Human beta-endothe	Sequence encoded b	Human acidic fibro	Fibroblast growth	FGF-1. Home sapie	Human endothelial	Fibroblast growth	Fibroblast growth	Human FGF-1 protei	Human endothelial	Fibroblast growth	FGF-1, SEQ ID NO:1	Human fibroblast	=	FGF1 protein. H	Human scidic fibro	Human fibroblast	Human fibroblast	Human fibroblast	Protein of human	Protein of human	Human mendie FGF	Numer PECGF accords	Human endothelial	Fibroblast growth	Human fibroblast	Human fibroblast	Recombinant human	Human (Gly93) aFGF	Human fibroblast g	Human FGF-1 protei	Murine fibroblast	Recombinant human	Human acidic fibro	Human aPGF encoded	Sequence of human	Human acid fibrobl	Human acidic fibro	Human acidic Fibro	Human recombinant	Human scidic fibro
		II.	AAMO6816	33W04805	AAW75414	AAW92283	AAP70482	AAP94037	AAR80776	AAR70812	AAHTS41S	AAW75711	AAW53022	AAYO8584	AAM92291	AAB10297	AAY90410	AAY32333	AAB85812	AAB61661	AAB50273	AAB50298	AAB50705	ABB99120	AA019990	AA019994	AAU76943	ABPS4277	200000000000000000000000000000000000000	AAW71363	AAY96879	AAU1117	AAR25570	AAWOOS61	AAG65647	AAE18806	AABSSSO	AAP90074	AAR05315	AAR05789	AAP70995	AAP90068	AAR25914	AAR34497	AAR74647	AAMO4806
			17	12	57	30		10	9	16	19	13	13	20	0	21	77	77	33	33	ä	23	55	53	53	53	2		1:	1 51	Ħ	53	2	17	22	23	33			7	ю	10	Э	Ä	16	77
		Match Length DB	154	154	154	154	155	155	155	155	155	155	155	155	155	155	155	155	155	155	155	155	155	155	155	155	155	155	269	156	156	156	155	155	153	153	155	154	154	151	140	740	140	ţ	100	140
*	Guery	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	200.0	100.0	100.0	100.0	100.0	100.0	1.00	100.0	100.0	100	98.7	98.7	7.86	7.76	7.76	96.2	96.2	95.8	94.8	83.8	92.0	91.8	91.8	91.8	97.8	97.8	91.8
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ALIGNMENTS

Botine bein-endothelial cell growth factor (bein-gord ANA0059) having an act of other score that a solid free both as a lart of the case and the case and extention of the case and the cas

Sequence 154 AA;

RESULT 1
AAMOGE16
ID AAMOGE16 mtandard; Protein; 154 AA.
AC AAMOGE16;

Ouery Match
Best Local Statistics 100.04; Score #35; TB 17; Length 154;
Best Local Statistics 100.04; Pred. Mc. 3.5-44;
Matches 344; Conservative O; Misharches 0; Indels 0; Gaps 0; Human recombinant end-th-first) call growt factors (GOS) here
Modestis and anhab (Modest) differ cally at their R-terminal endmay can be produced in transformed productive to their R-terminal endmay can be produced in transformed productions, respectively) derived
from the complete bound COT (MASS) and MASS (SA) respectively) derived
from the complete bound COT (MASS) and MASS (SA) respectively
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the processin. GOS above untility in the growth and emplification
treat damaged blood versult and other entochialist call include
the currentes, and no have almost approach applicable in the contract of the field.) Isolated, purified, biologically active bowine beta endothelial cell growth factor - useful to regenerate or treat damaged blood vessels Endothelial cell growth factor; ECGF, blood vessel; regeneration; hepstil-Schhouse siffnilty dhromatography; probe; oligonucleotide; FOFF, filtochiane growth factor. Recombinant human endothelial cell growth factors - for treating damaged blood vessels, etc. 121 WEYGLKKNGSCKRGFKTHYGORALIEBELFVSSD 154 Endothelial cell growth factor-beta; ECGF-beta. Human beta-endothelial cell growth factor. Human endothelial cell growth factor-beta. Burgess W. Drohan WN. Jaye M. Maciag T. (RHON) RHONE POULENC RORER PHARM INC. (RHOM) RHONE POULENC ROKER PHARM INC. RESULT 2 AAM04805 ID AAM04805 standard; Protein; 154 AA. Claim 1; Column 16; 22pp; English. Disclosure, Fig 8; 28pp; English. 18-DEC-1887, 87US-0134499, 03-MAR-1886, 86US-083594, 22-APR-1991, 91US-0839859, 03-NOV-1894, 94US-0334884, 03-NOV-1994; 94US-0334884. 87US-0134499. 86US-0835594. 91US-0693079. 91US-0734884. 94US-034884. 07-JUN-1995; 95US-0472964. 25-MAR-2003 (updaced) 29-DEC-1996 (first entry) 25-MAR-2003 (updated) 17-MAR-1997 (first entry) Burgess W. Maciag T. WPI; 1996-412132/41. N-PSDB; AAT37503. WPI; 1996-505421/50. N-PSDB; AAT45983. Sequence 154 AA; 18-DEC-1987; 03-MAR-1986; 29-APR-1991; 27-NOV-1991; 03-NOV-1994; 07-JUN-1995; Home sapiens. 03-SEP-1996. Home sapiens. USS552528-A. USSS71790-A. 05-NOV-1995. AAWO4805;

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Query Match
100.09; Score 225; DB 13; Length 154;
Marches 124; Conservative 0; Fred V. 5.5e-46; Indels 0; Gaps 0;
Marches 124; Conservative 0; Missarches 0; Indels 0; Gaps 0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This requires represents the auton raid desired of the autone beams there are adealable field great factor the ECOT. This amino acid sequence is identical to the alpha-ECOT but the best sequence constitution acids. The sequence was included from a hostin as no SCT. Obserminal amino acids. The sequence was included from a humb frain sequence and LOMA library using a proced designed based on transmiss of the bortine ECOT (see AMY7346-877343). The SUGRED process in can be used in compasition for processing would healing. ECOT is also used to grow colls on a prochabilite device our and any acid of the sequence of the compasition for processing would healing. ECOT is also used to grow colls on a prochabilite device our acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human beta-endothelial cell growth factor (ECOF) protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Compositions for promoting wound healing - containing endothelial cell growth factor polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, endothelial cell growth factor; ECGF; brain stem; probe; hybridkation; bovine; wound healing; prosthetic device.
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                                                                                                                                                            121 MFVGLKKNGSCKROPKTHYCOKALLFLEDEPVSSD 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Human beta-endothelial cell growth factor.
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AAM92283
ID AAM92283 standard; protein; 154 AA.
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AAN75414
ID AAM75414 standard; protein; 154 AA.
XX
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87US-03134499,
91US-0691079,
94US-0799659,
94US-0334884,
95US-0472964,
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86US-0855594.
87US-0134439.
91US-069079.
94US-0334884.
95US-0472964.
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                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-1959 (first entry)
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03-MAR-1986;
18-DEC-1987;
22-APR-1991;
27-NOV-1994;
07-JUN-1995;
11-APR-1997;
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03-MAR-1986;
18-DEC-1987;
29-MR-1991;
27-NOV-1991;
03-NOV-1994;
07-JUN-1995;
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Query Match 100.04; Score 825; DB 8; Length 155; Best Local Stailarty 100.04; Press No. 3.64-8.05 inches 156; Conservative O; Missarchies O; Indels O; Gaps O;
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Best Local Statisticy 100.0%; Pred. Mo 5.5-6-6; Indela 9; Gapa 9;
Matches 154; Conservative 0; Mismatches 0; Indela 9; Gapa 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence encoded by complete cDNA sequence of human endothelial cell growth factor (ECGF).
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MANDOL
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AAP94037;
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This represents the mains acid expense of human beta-solubitial call growth according to The investing a size freed to the amoding highs or beta-stor and plantin or existing the Wisered to the modeling highs classified signal profits and recognizing the Wisered to The Wise societies of classifier signal profits and report the signal peptide and recognized to the signal peptide to the first of the first of the first the signal peptide to provide a secondariant bird remains with care be used in present a secondariant blood vessels or other care the signal with adopting a secondariant calls.

DNA encoding a cleavable signal peptide and an embothelial cell growth factor - useful for producting recombinant embothelial cell growth factor proteins

WPI; 1999-069734/06.

100.0%; Score 825; DB 17; Length 154; 100.0%; Pred. No. 3.5e-84; Indels 0; Gaps 0; tive 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
Best Local Similarity 100.00
Matches 154; Conservative

Claim 1; Column 16; 23pp; English.

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Nime-difference 22..155
/note= "coxresponds to Alpha-2COF (AAM75413)"
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03-MAR-1986;
18-DBC-1987;
29-APR-1991;
27-NOV-1991;
03-NOV-1994;
07-JUN-1995;
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Query Match
100.01; Score #35; DB 16; Leugth 155;
Matches limitarity 100.01; Pred. McD. 1.6-6-40; Indels 0; Gaps 0;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
                                                                                                                                                                                                                                                                                                                                                                                     Owery Match 100.04; Score 15; DB 10; Length 155; Best Local Stallariy 100.04; Pard. Mo. 3.6-44; Matches 154; Conservative O. Mismatches 0; Indels 0; Gaps 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SAESVOEVYIKSTETGQYLAMDIDOLLYGSQTPNERCLFLERLEENHYYTYISKKHAERN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New conjugates of growth factor receptor liquid and translated upon to partic. Who or growth are to control cell proliferation in the easy, e.g. to prevent growth of presygial and corneal clouding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conjugate; fibroblast groath factor; 70%; cytotoxin; aspoxin; eye; cell profiferation; regulation; peerlygia; connest clouding; cencer; peerlast; fhoumatoid artititis.
                                                                                                                                                                                                                      Recombinant DNA encoding new fibroblast growth factor analogues - useful eg for accelerating wound healing and to control neowaecularisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baird JA, Houston LL, Nova MP, Sosnowski BA;
                                                                                                                                                                                                                                                                                                               See also AAP94038.
(Updated on 25-MAR-2003 to correct PA field.)
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AAR 0776 * tandard, Protesin, 155 AA.
XX
XX AAR80776;
AC AAR80776;
                                                                                                                                                  Fiddes JC, Abraham JA, Protter A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fibroblast growth factor 1, FGF-1.
                                                                                                                                                                                                                                                                                  Disclosure; Page -; App; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0213447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-1995; 95WO-US03448.
                                                         06-JUL-1988; 88EP-0306158.
                                                                                 07-JUL-1987; 87US-0070797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAY-1996 (first entry)
                                                                                                                 (BIOU ) BIOTECH RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PRIZ-) PRIZM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPX; 1995-336820/43.
                                                                                                                                                                             WPI; 1989-009785/02.
N-PSDB; AAN93088.
                                                                                                                                                                                                                                                                                                                                                        Sequence 155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9524928-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-1994;
15-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-1995.
                            11-JAN-1989.
EP298723-A.
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96US-0743261. 86US-0835594. 87US-0134499. 91US-0799859. 94US-0334884.

96US-0743261.

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Query Match
100.04; Score #25; DB 16; Length 155;
Best Local Similarity 100.04; Preed Wool, 16-e46;
Matches 124; Conservative 0; Indels 0; Gaps 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           would (taken procedure comprise for littled to sepecta.) FOF-1 to -1 may be used, pref. [For-1 the pref. ] to the pref. [For-1 the pref. ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGF.1; fibroblast growth factor; cytotoxic conjugate; fusion protein; sapozin; cytostatic; tumor; diabetes; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //note= "meguence of human fibroblast growth factor is homologous to the protein whose sequence starts at this position"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New monogenous preparations of cylotoxic conjugates and DNA -
contain fibroblast growth factors and cylotoxic agents for
treating TOP conditions such as tumours, disbettes and theumstoid
arthrits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, endothelial cell growth factor; EGGF, brain stem; probe; hybridisation; bovine; wound healing; prosthetic device.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key Location/Qualifiers
Misc-difference 2..155
Misc-difference 2..155
//note= "corresponds to hets-ECGF (AAM75414)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human endothelial cell growth factor precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'notes "Cys may be replaced by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 132 / Increase / 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 MFVGLKRNGSCKRGPRTHYGGRAILFLPLDVSSD 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PRIZ-) PRIZM PHARM INC. (WHIT-) WHITTIER INST DIABETES 4 ENDOCRINOLOGY.
                                                                                                                                                          121 WEVGLKRAGSCKROPKTHYGOKALLFLPLPVSSD 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 108-109; 128pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
AAR70812
ID AAR70812 standard; protein; 155 AA.
XX
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01-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | MAR70812|
| MAR70812|
| MAR70812|
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| MAR70813|
| MAR718R MAR718R MAR70813|
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Human scidic fibroblast growth factor,

25-JUN-1990 (first entry)

Acidic fibroblast growth factor.

Home sapiens.

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Ouery Mach 100.04; Soure 825; DB 19; Length 155; Bet Local Similarity 100.04; Pred. No. 3.04.05 10.04; Pred. No. 3.04.05 134; Conservative 0; Histories 0; Indels 0; Gaps 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the complete amino acid sequence of the human endochaid acid yearch factor (1967). The process as further processes to generate the beta-EGOP (strating from Aia as position 2; AMPSI4) and Aipha-EGOF (strating from Aia as position 2; AMPSI4). When the beta-EGOF (strating from Aia as position 2; AMPSI4). When the beta-EGOF is ileaved with trypain, the resulting Neterminal sequence is still fitting in equal to the processing variety appeared as included from a human beam or security of the processing variety appeared and included from a human beam or security of processing variety and the processing variety hashing. EGOF is also used to grow calls on a processing variety and the processing variety of the processing variety and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.04; Score #15; DB 19; Length 155;
Query Match
Per Local Similarity 100.04; Pred. No. 3.46-44;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fibroblast growth factor mutein and DMA - having reduced receptor binding and able to bind hoperin, useful for treating and regulating hepatic-railed disorders e.g. thromboats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 102
/nore- 'Giu-102 may be replaced by another smino
acid (Glaim 7), preferably Ala, 639 or Ser'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 107

//oce - 'Anno 'Day be replaced by prother with the control of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 110

//occ - *Am.110 may be replaced by moother meino

Gly, Met. Lea or fly. sepecially Ala. Gly

or See.
                                                                                                                                                                                                                                   Compositions for promoting wound healing - containing endothelial cell growth factor polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /noces "Phe-100 is replaced by another amino acid
acid (Claim 3), preferably Ala, Phe, Ser,
Gly, Mcr, Leu or Tyr, especially Ala, Gly
or Ser*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fibroblast growth factor-1; PGP-1; mutain; protein engineering; heparin; thrombosis; thromocytopenia; ophthalmic disorder; human; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burgess M. Drohan WN. Jaye M. Maciag T;
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AMPSTIL 10

AMPSTIL STANDARD PROCESS AND.

AMPSTIL STANDARD PROCESS AND.

E THOUSIAGE STOWN (ACCOUNTY)

PRINCIPLE STOWN (ACCOUNTY)

PRINCIPLE STOWN (ACCOUNTY)

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MANISTIC S
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MPI; 1998-594032/50.
N-PSDB; AAV34350.
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Query March
100.04; Score 425; DB 19; Length 155;
Bert Local Similarity 100.04; Pred. Mo. 1.6-6-64;
Rarches 18; Conservative 0; Mismatches 0; Indels 0; Osps 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fibroblast growth factor (FGP) proteins (AA95021-M51051 and AA85021-M51051 and AA85021-M5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel human Exhediate grout (actor, PROSI), also known as Exhediate growth Actor-19 (PGF-19). The nucleic entide, seations and polyappictae disclosed may be used in the dispensal and treatment of cumours and/or conditions absected by wendlation of PROSI POSITION or in the preparation of compositions for much the compositions for much the preparation of compositions are much than the much th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO533) POF-19: (Shroblast growth factor; human; diagnosis; treatment; rumour; neeplastic esh growth; cell proliferation; trumorgenesss; cencer; astocartes signaling; FOF-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGP; cell growth; survival; differentiation; central nervous system; peripheral nervous tissue; treatment; diagnosis; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding fibroblast growth factor - 19, useful for the disgnosis, prevention and treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New (throblass growth factor homologous factors - useful for, e.g. developing product for diagnoss and tractment of conditions developing product for diagnoss. We and neoplastic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botstein D, Goddard A, Gurney Ab, Hillen KJ, Lewzence DA;
Roy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 11, 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fibroblast growth factor protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY08584 standard, Protein, 155 AA.
                                                                                                                                                                                                          RESULT 11
AAM53022
ID AAW53022 standard; Protein; 155 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PGF-1 protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-NOV-1998; 98WO-US25190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-1997; 97WO-US15237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-1998; 98US-0158432.
25-NOV-1997; 97US-0066840.
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100.01; Score 825; DR 20; Length 155;
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growth factor - useful for producing zecombinant endothelial cell
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Note- "acidic-PGF begins at this position"
22
/note- "alph-ECGF begins at this position"
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This invention describes a novel human kratinocyte growth fastor, NGF-2 (1), which has antiliotes, antidiates, and antidiates and continue there much a continue that the sales useful for freeting inflammatory boat district and continue there are antidiates, and antidiates, and antidiates, and antidiates, antidiates, and antidiates, antidiat
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Ouery Match

Bert Local Similarity 100.0%, Pred. No. 1.6-04.0

Bert Local Similarity 100.0%, Pred. No. 1.6-04.0

Bert Local Similarity 0. Mismatches 0, Indels 0, Gaps 0;

Marches 18, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
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Dillon PJ, Gentz RL, Ruben SM, Zhang J, Moore PA, Rumpy MA;
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                                                                                       Chandler LA, Somnowski BA, Baird JA;
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97US-0039045.
97US-0055561.
95WG-USD1790.
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28-FEB-1997;
13-AUG-1997;
05-MN-1995;
14-FEB-1995;
23-MAY-1997;
13-AUG-1997;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 11, App. Sequence 6, App. Payments 6, App. Sequence 6, App. Sequence 9, App. Sequence 7, App. Sequence 6, App.	6 of USE 1 meloth 155; 1 meloth 155; 1 meloth 155; 2 meloth 156; 3 meloth 156; 3 meloth 156; 4 meloth 156; 5 meloth 156; 6 meloth 156; 6 meloth 156; 7 meloth 156; 8 meloth 156; 8 meloth 156; 9 meloth 156; 1 meloth 15	ссен.
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Query Match
100.04; Score 875; DR 2; Length 155;
Match Local Similarity 100.05; Fred No. 3.14-97; Indials 0; Ospe 0;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Ospe 0;

REFERENCE/DOCKET NUMBER: 325800-438 TELECOMMUNICATION INFORMATION:

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US-09-718-904-10
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100.09; Score #35; DB J; Length 155;
Best Local Similarity 100.09; Presh No. 3.10-70;
Matches 134; Conservative O; Klamatches O; Indels O; Gaps O;
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Best Local Statisticy 100.04; Score #35; DB 9; Leugth 135;

Best Local Statisticy 100.04; Pred, No. 31-e-97; Indels 0; Gaps 0;

Matches 134; Conservative 0; Missarches 0; Indels 0; Gaps 0;
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/ MOLECULE TYPE: protein US-09-023-082A-16

Query Match 100.00; Score 825; DW J; Length 155; BW Best Local Similarity 100.00; Pred. No. 11-40.00; Dred. Whither 314; Conservative O; Missarches O; Indels O; Gaps O;

INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 1.55 amino acids TYPE: amino acid STRANDEDNESS: mingle

TOPOLOGY: Linear MOLECULE TYPE: protein FRACHENT TYPE: internal US-09-086-628-4

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Best Local Stellarity 100.01; Score 23; DB 4; Length 155;
Best Local Stellarity 100.01; Pred, Mo. 1.14-40.01
Hetches 154; Conservative O; Kleanstolles 0; Dadels 0; Gage 0; August 14, 2003, 10:27:24; Search time 56 Seconds (without alignments) 360.259 Million cell updates/sec Pred. Mo. :a the number of results predicted by chance to have a core greater than or equal to the acces of the result being printed, and is derived by analysis of the total score distribution. US-10-022-554A-4 825 1 ABGEITFFRALTEKFMLPPG......PRIHVGQKAILFLPLPVSSD 154 ADDRESSEE, SEED and REENT LIP

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COUNTRY, 18 ALG GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. Total number of hits satisfying chosen parameters: 492763 seqs, 131003257 residues Search completed: August 14, 2003, 10:28:04 Job time: 19 secs Post-processing: Minimum Match 0% Maximum Match 100% Limting first 45 summaries OM protein - protein search, using sw model Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Minimum DB seq length: 0 Maximum DB seq length: 200000000 Title: Perfect score: Sequence: Database : Searched: Run on: q ò

Sequence 8, Appli Sequence 9, Appli Sequence 3, Appli Sequence 3, Appli Sequence 9, Appli

Description

Sequence 1, Appl. Sequence 1, Appl. Sequence 2, Appl. Sequence 3, Appl. Sequence 3, Appl. Sequence 3, Appl. Sequence 3, Appl. Sequence 4, Appl. Sequence 4, Appl. Sequence 5, Appl. Sequence 5, Appl. Sequence 6, Appl. Sequence 1, Appl. Sequence 11, Appl.			Length 154; Indels 0; Gaps 0;	ILPOATUOTRASDOHIOLOL 60	Ė	Length 154; Indela 0; Gapa 0; ILROCYTONESSIONIQUE 0; IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
9 06.00 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	ALIGNMENTS	9992945 "Y A. Lan I. L	.0%; Score B25; DB 10; .0%; Pred. No. 4.1e-84; 0; Mismatches 0;	HEPBAYXERLINGSMOHERE. HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIH	infockliffizers	0.0%; Score 835; DB 15; 0.0%; Pred. Mo. 4.1a-84; e. 0; Mismatches 0; PMLPOWYKKELINCSNOGHILAI
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Sequence 9, Appli Sequence 2, Appli

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Query Match 100.04; Score 415; DB 9; Length 115;
Base Local Skulharity 100.04; Pred 106.4.1.4-4.0.
Hatches 154; Gomestwaite 0; Namarches 0; Indels 0; daps 0;
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Query March 100.04; Score 825; DB 9; Length 155; Met Decal Similarity 100.04; Pred. Nov. 4.18-40; P. Marches 154; Conservative 0; Manarches 0; Indels 0; Gaps 0;
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Base Local Stallarity 100:04: Score 835; DB M6: Length 158;
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779.472 Million cell updates/sec

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Ribergia, A.; Tischer, E.; Graves, D.; Tumcho, A.; Miller, J.; Gespodarowicz, D.; Abraham, J.A.; Shipley, G.D.; Fiddes, J.C.
Ribergia, A.; Tischer, E.; Graves, D.; Tumcho, A.; Miller, J.; Gespodarowicz, D.; Abraham, J.A.; Shipley, G.D.; Fiddes, J.C.
A.; A.; Miller, Res. Commun. 164, 112-1123, 1389
A.; Miller, Structural analysis of the gene for human acidic fibroblast growth factor.
A.; Miller, Structural analysis of the gene for human acidic fibroblast growth factor and its expression in fetal tissues.
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Mesiathan: 1-17 oddy.
- Experimental source: brain
Goderschi, P. Tratec-Schoofer, M.; Bohlen, P.
188 Jett. 204. 203-207, 1986
188 Jett. 204. 203-207, 1986
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Chavan, A.J.; Haley, B.E.; Volkin, D.B.; Marfia, K.B.; Verticelli, A.H.; Brunar, H.H.; Draper, J.P.; Burke, C.J.; Middaugh,
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Afficient Historical of Indisorder with acidic fibroblast growth factor (FUF-1).
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Best Local Stallarity 100.01; Pred, No. 1.24-0.04
Matches 154; Conservative 0; Hismatches 0; Indels 0; Ospe 0;
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Bear Local Stallarity 95.5%; Pred No. 7.10-ed;
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C.Speciari Num 107-3153 | sequence revision 17-Apr-1593 | fext_change 16-301-3999

C.Rocension (D715-0) - 75531

E.Robert, J.W. 3 mailton, C.; Ooldfath, M.; Hamb, O.; Martin, G.R.
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Accession: A54539; WIID:#2187766; PMID:#2187762 Quary Match 22.1%; Score 760; DR 1; Langth 155; See the Carl Similarity 19:2; Fred. NO. 1.De-53; Matches 142; Conservative 6; Mananches 6; Indels 0; Gaps 0; 61 SABSVOBUYIKSTETGOYLAMDTDOLLYGSÇTPNEECLFLERLEENHYMTYISKKHAEKN 120 62 CARSIGEVYIXSIETOQPIANDTOGLYGGGTPNEECLFLERLEENNYTVISKKHABKH 121 A biologust repear spects.
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Query March 80.4%; Scote 746; DB 2; Length 155;
Dest Local Similarity 90.3%; Pred. No. 1.78-62; Thicks Narches 13; Conservative 8; Mirmatches 7; Indels 0; Gaps
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Best Local Similarity 90.34; Pred. No. 5e-62;
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A.Accession: SDR53

A.Rescute Operation procesh

A.Residues 123-10, X, 124, X, 46-46 RMIS>

C.Residues 123-10, X, 124, 46, X, 46-46 RMIS>

C.Residues 123-10, X, 124, X, 46-46 RMIS>
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A.Rosafeast and A.Rosafeast R.Useno, M.; Baird, A.; Sach, F.; Miss, M.; Guillemin, R.
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49.44; Score 408.5; DB 2; Length 189;

Matches Billwrith 13.7; Pred. No. 7.6e-3.1

Matches 3; Conservative 18; Mismatches 50; Indels 5; Gaps 2;

Matches 30; Conservative 18; Mismatches 50; Indels 5; Gaps 2; 49; Indels 5; Gaps 2; 58 LQLSABSVGEVYIKSTETGQYLAMDTDGLLYGSQTPNEECLFLERLEBNHYNTYISKKHA 117 1 AEGEITTFTALTERFN----LPPGNYKKPKLLYCSNGGHFLRILPDGTVISTRDRSDQHIQ 57 Abstract positionary
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Abstract Structure and Abstract ch 50.1%; Score 413.5; DB 1; Length 157; S4.5%; Pred. No. 2.6e-31; S5.5%; Pred. No. 2.6e-31; S5; Conservative 17; Mismatches 49; Indels 5; 118 BKNWPVGLKKONGSCKRGPRTHYOOKAILFLPLPVSS 153 118 EXMETVOLKNOSCKRGPRIHYGOKALLFLPLPVSS 153 124 -- SHYVALKRIGOYKLGPKIGPEGKAILFIPHSAKS 157 156 D--WYVALKRTGOYKPGPKTGPGGRAILFIPHSAKS 189 Query Match Best Local Si Matches 85;

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SES Lett, 204, 201-207, 1956
"This: Patrial molecular characterization of embothelial cell mitogens from human brain: acidic and basic fibroblarc growth
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A. Rickinger and Sci. V. A. s. S. Sci. 182-1840. 1999
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A. Ricking
N.Costesias basis (ibroblast growth factor, 1MK form
C.Specias 13.-01.2009 Samequence, revision 31.-06-1993 Text. change 21.-01.2000
C.Dates 31.-01.2009 Samequence, revision 31.-06-1993 Text. change 21.-01.2000
C.Accession: A3239; AG:537, A26462, B32074; SOC297; A54316; B54316; A33624; B2424); B2430; S42242; B55784; IS2267;
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Abraham, CA.1; Manay, CLL.; Tamolo, A.2; Marysta, A.7; Fiddess, C.C.
Abraham, CA.1; Manay, CLL.; Tamolo, A.2; Marysta, A.7; Fiddess, C.C.
Abraham, CA.1; Manay, CLL.; Tamolo, A.2; GST-66; JS66

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62 OLGARERGUVSIKGVCANRYLAMRIDCHILASKCYTERCFFERLESNWYNTVSRKUS-120
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Copyright (c) 1993 - 2003 Compugen Ltd.
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and is derived by analysis of the total score distribution.

SUMMARIES

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5 :	Jaye M., Howk R., Burgess M., Rican G.A., Chiu KM., Ravera M.M.,
5 !	O'Brien S.J., Modi W.S., Maciag T., Drohan W.N.;
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Ŀ	"An acidic fibroblast growth factor protein generated by alternate
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Schauff, "Shrama Ma., Schoor Ed., Schaper M.;
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REGLINE-ST4051; PubMed-2470029;
Foodstan S., Yan G.C., Bahrenburg K., Monason P.E.;
The nucleotide sequence of rat heparin binding growth factor 1
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21-007-1396 [Rel. 04]
21-007-1396 [Rel. 05]
21-
PREFIGURE STANDARD, PRT. 155 AA.

O.1581-1991 (R.1.) T. CLEAR-OIL

T. 21-7881-2901 (R.1.) T. CLEAR-OIL

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THORN N. BARTER A., Enc. P., Lings M., OLILlemin R.).
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Bordae, Captine, Ovia.
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MEDIO CENTRAL A. SHARMAN, S., Same O., Jacobe S.C., Lawson R.K.;
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Amainor takehead form human bening procentric hyperplastic tissue.";
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**Autechi P. Terter-Schooled H. Behlen P.;

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PROLIBERATORS, PARKELANZAS,
Abraham J.A., Mangalam, T.L., Thusbla A., Mergia A., Fiddes J.C.;
Thuman basis (Elbroblam growth factors nucleosides sequence, genomic organization, and expression in mammalam calls,;)
(3) Spring Nach, Symp, Quant. Biol. 51:857-688(1988).
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- A Com Of Mannah hasic fibroblast growth factor with an extended autochem. Biophys. Res. Commun. 144:551-550 (1997).
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T.Cioning and expression of CDMA encoding human basic fibroblass.
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"Adjumicacular mass forms of basic fibroblast growth factor are initiated by alternative CDG codens.";

Proc. Natl. Acad. Sci. U.S.A. 66:1836-1840(1983).
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Glemeter or 10-39.
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Glemeter od-Alige G. C. Com G., Marther V.B., Thomas K.A.;
Human beräll edgived actidic and basic (Election)ass growth factors;
sanior exertial sequences and specific attendant of extitutions.
Takinger Bookly, Res. Gemman. 185:541-546 (1946).
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MEDLINE-SALLISLS), PUBLICALLISSS, WAS NOW N. KREENDE Y.;
FORWIGH, Kitegraw K., FUSISHISH A., Mateura Y., Kateube Y.;
Cryetal atgueture of basic fibroblast growth factor at 1.6-A
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S. NASY CRYSTALLOGRAPHY (2.B ANGSTROMS).
MEDGINE-$1055983; PubMed-1702556;
Zhu X., Komiya H., Chirino A., Faham S., Fox G.M., Arakawa T.,
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SUGURNEZ FROM N.A.
PRODUZENSHASZI, Pheked-2538817;
PARCH M., Kajada M., Parce A.C., Klagabrun M., Lelias J.M.,
Likaurun P., Chalon P., Tauber J.P., Amakric F., Smith J.A.,
FT BINDING 119 122 HERARIN (POTENTIAL).
SQ SEQUENCE 158 Ah: 17374 MW; 78698684C17F1816 CRC64;
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J. Biochem, 110:360-363(1991).
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FEBS Lett. 213:189-194(1987),
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B.T., Ress D.C., co-dimensional structures of acidic and basic fibroblast growth

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APPENDENCE OF STRICKLARITY, BELCHES TO THE REPARLS-BINCHED GROWTH PARCENCE PARLIX.

CONTRIBUTION OF STREET-STREET HELDERS TO THE REPARLS-BINCHED GROWTH PARCENCE OF THE STREET-STREET HE STREET-STREET HE STREET-STREET HE STREET-STREET HE STREET-STREET HE STREET HE STREET-STREET HE STREET-STREET HE STREET-STREET HE STREET HE STREET-STREET HE STREET HE STREE SECULD SECULATE FROM N.A.

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0.72B-1936 (Rel. 31, Law sequence update)
19-78B-1937 (Rel. 31, Law sequence update)
19-78B-2037 (Rel. 41, Law annoten update)
19-78B-1937 (Rel. 41, Law annoten update)
19-78B-1938 (Rel. 41, Law annoten update)
19-78B-1938 (Release of March 2)
19-78B-1938 (Rel. growth factor] (Rog) (presentoph),
Monodalphie domestics (Short-tailed grey opensus).
Elebryota Hexico; Choddes; Creminer, Verebrier, Euchoorcom;
Musmallar, Mericais; Didephisorphia; Didephide; Monodalphia,
(NoT_marp-116); MONDO STANDARD; PRT; 156 AA. Query March Best Local S: Marches 82 8 q ò 셤

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107 7272 ABIT STANDARD; PRT; 137 AA.

107 1272 ABIT STANDARD; PRT; 137 AA.

108 1272 ABIT STANDARD; PRT; 137 AA.

109 1272 ABIT STANDARD; PRT; 137 AA.

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                                                                                                                                                                                                                 118 BXXWFVGLKROGSCKRGPRTHYGQKAILFLPLPVSS 153
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Meery March

Ages Local Stallarity S2.9% Pred. No. 1.2e-3; Indels 6; Gaps 2;

Matches 83; Conservative 17; Mismatches 5; Indels 6; Gaps 2;

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4.14; Scote 181; DB 1; Length 137;
Best Local Similarity 55.94; Pred, No. 14e-26;
Matchae 71; Conservative 16; Mismatches 39; Indelse 2; Gaps 1;
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131 GPSGIGAI 137
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Search completed: August 14, 2003, 10:26:31 Job time : 12 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

August 14, 2001, 10:24:23 ; Search time 37 Seconds (without alignments) 1074.057 Million cell updates/sec TITLE: US-10-022-554A-4
Perfect score: 025
Perfect score: 1 ARGELITERNEPRO.......PRINCONAIMFURDEPUSSD 154
Sequence: 1 ARGELITERNEPRO........PRINCONAIMFURDEPUSSD 154 Total number of hits satisfying chosen parameters: 830525 megs, 258052604 remiduem OM protein - protein mearch, using aw model Post-processing: Minimum Match Ot Maximum Match 100% Listing first 45 summaries Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Minimum DB weg length: 0 Maximum DB meg length: 200000000 Searched:

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Ouery Match	7.	49.0	48.3	46.6	46.5	45.2	43.5	39.6	39.3	97.9	36.4	36.4	36.1	35.5	34.2	33.3	31.3
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30.9	7.06	00.3	30.1	30.0	39.62	29.3	29.0	28.5	28.5	27.6	27.5	27.0	26.8	26.8	26.5	25.8	25.5	25.3	25.3	25.3	25.3	25.2	25.0	24.5	24.5	54.5	24.5
255	253	250	248.5	247.5	244.5	241.5	239	235	235	228	226.5	223	221.5	221	218.5	212.5	210.5	208.5	208.5	208.5	208.5	207.5	206	202.5	202.5	202	202

PRT; 106 AA.

PRELIMINARY;

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18 (1)

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THE THIND PRANCES FROM THE PROPERTY OF THE PROPERTY Omery Match
49.0%; Score 404.5; DB 4; Langth 196;
Marches 94; Conservative 16; Missanches 91; Indels 5; Gaps 2;
Marches 94; Conservative 16; Missanches 51; Indels 5; Gaps 2; Owary Match
4-13; Score 199-5; DB 13; Length 155;
Beet Local Stallarity 54-6; Pred No. 125-12;
Marches 63; Conservative 13; Manarches 45; Endels 5; Gaps 2; Owery Match
46.64, Score 384.5; DB 11; Length 153;
Best Local Similarity 54.9 Fred Abs C. 64.e.3)
Matchies D3. Conservative 17; Missarches 51; Indels 5; Gaps 3; 1 ARGETTETALTERPA.--LPPGMYKKPALYGSMGGHERALDDGTWGTRDSSOOHIG 57
43 AAGSTLIPHILEDGGGGGAFPGHFROFRALGGGGFFLKRIDGKWGVBESDOHIK 102 59 QLSAESVGEVYIKSTETGQYLAMDTDGLLYGSQTPNEECLFLERLEENHYNTYISKKHAE 118 62 QIQAREROVSIKOVCANRILANKEBORILAS-CVTEBCPFFERIESHWYNTYRSKKXS- 119 1 AEGELTTPTALTEKPN--LPPGAYKKPKLLYCSNGGHPLRILPDGTVDGTRDRSDQHIQL 58 2 AASGITSLPALPEDGAARPPOHRUPKUNKTKOOFFLRIHPDGRVDGVREKSDHVKL 61 MESTIN 3

MORPHON TO STRICT AND MORPHONE AND 10. 100513.3 PRELIMINARY; PRT; 153 AA.

(0.0752), T. T. DECC-2011 (TERRELICE.) 12. Created.)

TI 10.DECC-2011 (TERRELICE.) 13. Least sequence updates)

TI 10.DECC-2011 (TERRELICE.) 13. Least monotation updates)

Elibroblant growth factor 2. Least monotation updates)

Elibroblant growth factor 2. Least monotation updates)

Mrs waterilus (Fotors).

So Mansanary Markenson, Considera, Vertebrens, Rutalsonrout;

Mrsmallis, Eutheria, Rodentia, Gentrophachi, Markidae, Mutinae, Mus.

10. Least 20. L SEQUENCE 196 AA; 21203 MM; DGB5447137260343 CRC64; OSSERVA PRELIMINARY PRT; 155 AA.

OSSERVA CONTRIBUTED. 13, Created)

OLDEC-1001 (TERMELEAL) 13, Lear sequence update)

OLDEC-1001 (TERMELEAL) 13, Lear sequence update)

OLDEC-1003 (TERMELEAL) 13, Lear shinotation update)

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Query Match

16.5%; Score 1815; DB 13; Length 155;

Best Local Stallarity 13, 744 (No. 18.4-1);

Matches 80; Conservative 19; Missarches 5; Indels 5; Gags 2;
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2 TITUSTICA CAL. JOSEPH 2. INSERTE J.;

2 TITUSTICA CAL. JOSEPH 2. IN THE PROPERTY OF THE 
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55.3%; Pred. No. 7.5e-30;
tive 17; Miswatches 40; Indels 2; Gaps 1;
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01.307.1376 (TERMINAL) 102, Greated)
01.307.1376 (TERMINAL) 103. Les emperors update)
10.307.1376 
Cynoge pyrzhogaster (Japanese common newt).
Bukaryoni Metanoa: Chordete, Cranistr, Verebrate, Euceleostomi,
Ambhisis, Battenchis, Caudeta, Salamandroides, Salamandrides: Cynope.
MCB_TaxID=8330;
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Cania familiaria (Decembera) Craniara; Vertebrata; Bureleostomi;
Nemania; Eutheria; Carnivora; Fissipedia; Canide; Cania.
REB_TacID-9615;
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Best Local Similarity 55.3%
Matches 73, Conservative
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Query Match
Best Local Similarity 98-13+; Score 324; DB 6; Length 62;
Best Local Similarity 98-4; Prest No. 2,5s-25;
Best Local Similarity 1, Wismarches 0; Indels 0; Gaps 0;
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HEIGHES-SCHOOLS, PubMed-190434).
The ARL FA. Hisher H. Frise W.E., Miller G.G.,
"The appression of science threebase growth forcor (heparis-binding colls.").
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Equis caballus (Horse).
Memalis, Extheria; Perissodactyla; Equides; Equis.
MEB_Tax[De5736].
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0.1004.200 (TERRENAL D. Lame sequence update)

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Acidic Cibrollant growth factor (Terquent)

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37.99; Score 313; DB 4; Length 59;
Best Local Similarity 100.09; Pred. No. 3e-24;
Matches 58; Conservative 0; Mismatches 0; Indels
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Osepta PRELIMINARY Front,
Os. DEFACTOR CERRELEAL 21. Cected of Companies
Os. MRX-2000 (TERMELEAL 22. Lear sequence update)
Os. MRX-2000 (TERMELEAL 22. Lear sequence update)
Fibroblast growth factor 1. (Fragment)
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QUURALI OL-MAY-2000 (TERBELER 13, Created)
OL-MAY-2000 (TERBELER 13, Late agenore update)
OL-MAR-2000 (TERBELER 12, Late annoration update)
Acidic fibroblast growth factor (Fragment).
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119 LPMSAKS 125
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Query Match
38.64; Score 327; DB 13; Length 125;
Best Local Smillarity 52.84; Pred. Mo. 3.14-32;
Montholes 67; Conservative 16; Missacches 42; Indels 2,

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Beet Local Similarity 100.39; Prod No. 6.2e-23;
Matches Si; Conservative 0; Mismatches 0; Conservative 0
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Base Local Similarity 100.04; Pred. No. 6.10-23;
Machine Similarity 100.04; Pred. No. 6.10-23;
Machine Si; Conservative O; Mismatches O; Lindels O; Gaps
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FT NOW, TER 59 AA; 6595 FM; SC&JDIE64847148A CRC64;
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1827.218 Million cell updates/sec

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SUMMARIES Result Query
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	4 825	100.0	481	φ	I08499	I08499 Sequence 13
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	7 825	100.0	490	o	HSAFGF	X65778 H.sapiens a
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-	16 825	100.0	1073	ø	BC032697	BC032697 Homo sapi
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17	157 757	91.8	÷	9	105317	I05317 Sequence 3
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		1.06	468	10	GGU31863	U31863 Gallus gall
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đ	49	64 AACTACAAGAAGCGGAAACTGCTGTACTGCTCCAACGGTGGTCACTTCCTGCGTATCCTG 12:	m
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š	no.	81 MetAmpThrAmpGlyZewIewTyrGlySerGlnThrProAmmGluGymLewPheLew 100	٥
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ď	42	424 CAGAAAGCTATCCTGCTGCCGGTTTCCTCCTGAC 465	
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REFERENCE		1 (bases 1 to 468)	
AUTHORS	ORS	Stegmann, T.J., Kordynm, V.A., Slavchenko, I.Yu., Chernykh, S.I. and	
a alexan		Vozianov, O.F.	
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121 TrpPheVakGlyLeuLysLysAsnGlySerCysLysArgGlyProArgThrHisTyrGly 140	402 TGGTTTGTTGGCCTCAAGAAGAATGGGAGCTGCAAACGCGGTTCTCGGACTCACTATGGC 461	141 GlnLysAlaileLeuPheLeuProLeuProValSerSerAsp 154	462 CAGAAAGCAATCTTGTTTTTCTCCCCTGCCAGTCTCTTCTGAT 503
121	4 02	17	462
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Search completed: August 25, 2004, 00:24:39 Job time : 3657 mecs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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August 24, 2004, 21:08:03 ; Search time 376 Seconds (without alignments) 1739.953 Million cell updatos/sec Run on:

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Scoring cable: BioSiM62 , Kgapext 0.5 Xgapext 0.5 Ygapext 0.5 Ygapext 0.5 Ygapext 7.0 Ealop 6.0 , Pgapext 7.0 Ealop 6.0 , Delext 7.0

Total number of hits satisfying chosen parameters: 3373863 megm, 2124099041 residuem Minimum DB seq length: 0 Maximum DB seq length: 200000000 Searched:

Post-processing: Minimum Match 00* Maximum Match 100* Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a soone generar than or equal to the score of the result being printed, and is derived by smallysis of the cocal score distribution.

ID Description	AAT45983 Auman end	AN92890 Ann92890 Synthetic	ABV78179 Human DNA	Abz35755 Human pol.	BX09998 Human DNA	ARK98918 Ank98918 Human aci	IBL91720 Human pol	AAN71029 Sequence	AAN90994 Partially	UNGOSH71 Amq03871 Synthetic	ABK10592 cDNA endo		AAN70788 Complete	AAN93088 Acidic fit	AAT37503 Human bet	AAV34350 Auman end	
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ALIGNMENTS

В	ID AAT45983 menndard; cDNA; 462 BP.
×	
Ų	AAT45983;
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늄	25-MAR-2003 (revised)
ä	17-MAR-1997 (first entry)
ŭ	
30	Human endothelial cell growth factor-beta cDNA.
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ž	Endothelial cell growth factor-beta; ECGF-beta; da.
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So	Homo sapiens.
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N.	USS571790-A.
ğ	
G	05-NOV-1996.
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i.	07-JUN-1995; 95US-00472964.
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a.	03-MAR-1986: 86US-00835594.
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ď	(RHON) RHONE POLIZENC RORER PHARM INC.
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н	Drohan MN, Jaye M, Maciag T, Burgess M;
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젎	MPI; 1996-505421/50.
DR.	P-PSDB; AAWO6816.
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E.	Recombinant human endothelial cell growth factors - for treating damaged
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ار	Control of Control of the Control of
g	name endochellal cell growen ractors (
ы	(AAM06816) and alpha (AAW06817) in transformed prokaryotic or eukaryotic
8	host cells. The sequences are derived from the complete cDNA (see also
S	AAT45985) for human EGGF, obtd. from a brain stem cDNA library. The 2 DNA
į,	can be utilised
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Score: 8.55.00
Percent Similarity: 100.004
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US-10-022-554A-4 (1-154) x AAT45983 (1-462)

1 AlaGluGlyGluIleThrThrPheThrAlaLeuThrGluLysPheAsnLeuFroProGly 20		1 OCTGAAGGGGAAATCACCACCTTCACAGCCCTTGACCGAGAAGTTTAATCTGCCTCCAGGG 60
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49	Prokap01yThrValkap01yThrArgkapArgserkap01nHfs11c01nLeuGh1keu
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ò f	61 Serkladludsrvaldlydluvaltyriletysferfingliffieldydhytheulla 80
à à	MethapThiAmpGlyLeuLeuTyrGlySerGlnThirProAmnGluGluCysLeuPheLeu 1
台	241 ATGGACACCGACGGCTTTTATAGGGCTCACAGACACCAAATGAGGAATGTTGTTGTTCCTG 300
79	101 GlukrgLeuGluclukanHiaTyrkanThrTyrlleSerLysLysHisAlaGluLyskan 120
a	301 GAAAGGTTGGAGAACCATTACAACACCTATATATCCAAGAAGCATGCAGAGAAAA 360
ò	121 TrpPheValGlyLeuLysLysAsnGlySerCysLysArgGlyProArgThrHisTyxGly 140
g	361 TOGITIOTIGOCCTCAAGAATUGGAGCTGCAAAGGCGGTCCTCGGACTCACTATGGC 420
70	ClnLysklalleLeuPheLeuProLeuProValSerSerAsp 1
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AAN928	06
0 × 2	AM92890 standard; DNA; 465 BP. AAN92890;
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44	25-MAR-2003 (xevised) 22-JIN-1990 (first entry)
z z	Synthetic gene encoding human acidic fibroblast growth factor.
X X	Acidic fibroblast growth factor; ss.
XX OS	Synthetic.
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EE	/*tag* c /label* code
EE	/notes may also be ACT" misc feature 28, .30
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X	J000 (806T-190-
PR.	26-JUN-1987; 87DE-03721081.
a	(PROG-) PROGEN BIOTECHNIK GMBH.
¥ II	Gruss P. Knoerzer W. Schnolze M. Rackwitz HR;
X K	MPI; 1989-008572/02.
×	genes encoding acidic and h
2 2	is with mitogenic and angiogenic activities.
¥ 2 1	Claim 3; Page 19; 20pp; German.
X 8	This DNA sequence encodes human scidir (ibroblast growth factor. The gene
រ ខ <u>រ</u>	is closed in plasmid DIASO3 and expressed in E. coli. The recombinant
8 8	polypeptides thus produced mave mitogenic activity, making them userui as additives for cell culture media, and have anglogenic activity, making
88	them useful in wound healing and organ transplants. See also AAN92889 and AAN92891. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
ខម	MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
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å à	4 UCTURAGGITARATTATURUTATURUTGUTTIKATUGUTTIKATUGUARAGITIKARUTITERUTTIK 93 21 AmniyriysiyelyelrolyeleuleulyrCysSexAmnGlyGlyHimbheleukrglleleu 40
	41 ProkapolyThrValkapolyThrArgkapArgSerkapolnHisIleGlnLeuGlnLeu 60
ą	124 CEGGACGGIACCGTTGACGGTACCCGTGACCGTTCCGACCACCACATCCAGCTGCAACTG 183
	61 SerAlaGluSerValGlyGluValTyrIleLysSerThrGluThrGlyGlnTyrLeuAla 80
	184 TCCGCTGAATCCGTTGGTGAAGTTTACATCAAATCCACGAGACCGGTCAGTACCTGGCT 243
	81 NetkapThrAapGlyLeuLeuTyrGlySerGlnThrProAsnGluGluCysLeuPheLeu 100
đ	244 ATGGACACGGACGGTGTGTGTTCCCAGACGCGAAGAAGAAGATGCTGTGTTCCTG 303
	101 GludrgLeuGluGludanKisTyrAsnThrTyrIleSerLysLysHisAlsGluLysAsn 120
용	304 GAACGTCTOGAAGAACCACTACAACACCTACATCTCCAAGAAGCACGCTGAGAACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA
8 8	121 TEPRAVALOLYGOULYALYSANOLYSOKCYALYAAKEGLIYEKOAKEGTHAEKATYKOLY 140
à	GlnLymalalleLeuPheLeuProleuProValSerSerAmp 154
â	CAGAAAGCIATCCTGTGCGGTGCCGGTTTCCTCGGG
NT B	.f. 3. 587-3879 = mandard: DNA; 468 9P.
	V78179;
	15-NOV-2002 (first entry)
	Human DNA SEQ ID NO 63.
	RNA inhibition; deRUAl; gene expression inhibitor; oncogene; cytostatio; virucide; protocoscide; gene; de.
	no sapiens.
	WO200255693-A2.
	18-JUL-2002.
	09-JAN-2002; 2002MO-EP000152.
	-JAN-2001, 2001DE-01000586
	25-677-201, 2011E-0105530. 25-707-201, 2011E-01056411. 07-DEC-1001; 2001DE-01060151.
	IBO-) RIBOPHARMA A
	Kreutzez R. Limmez S., Rost S., Hadwiger P:
	WPI; 2002-590671/63.
181	Inhibiting expression of rarget gene, useful e.g. for inhibiting oncogence, by mainimizating double-extraded RNs complementary to the taxper and having an overlang.
	Claim 10; Page 147; 203pp; German.
	The invention relates to inhibiting expression of a target gene (I) in a second of the
	cell by introducing an innibitory and (usawal) making a double-stranged structure of a most 49 consecutive bases. At least part of one strand fact of Admin is constituted by (1) and at least and at least of the strand
	(set) or descent is comprehensive of the matthe is seen one and of descent has an overhange of 1-4 nucleotides. The method is used to inhibit the proviseion of a wide transmission of numes. A concesses expedite names are
	opposite the same range of general above the properties of contraction of the parties of the properties of the propertie
	ARRNA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the
	effective concentration inside the cell. The present sequence is that of a gene related to the invention
	Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 other;
Бų	0.0-02 Length.
	1.336-34 198

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CC gene fragments weed to illustrate the method of the invention SQ Sequence 468 BP; 131 A; 135 C; 126 G; 96 T; 0 U; 0 Other;	on age fragments used to illustrate the method of the invention So Sequence 468 BP; 131 A; 115 C; 126 G; 86 T; 0 U; 0 chee; Alignman Socree; The first force: 1.308-34 Length: 468	888	interferon great expression of th	Ty increases the target genes,	and the effect	ch deRNA can inhibit is even greater when ds
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The invention relates to a method for inhibiting expression of a target congression price (Alliches-Alliches) in a cell by introducing at least one of the constraint of the traper goes and has at least one ond a single constraint with the traper goes and has at least one ond a single constraint with the traper goes and has at least one ond a single constraint with the traper goes and has at least one ond a single constraint with the traper goes and has at least one on a single constraint of the constraint of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting gene expression in cells, useful for e.g. treating tumors, by introducing double-stranded complementary obligoRNA having unpaired terminal bases.
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Pameodium; virum; viroloi, oytokine; prinn, maltense oligonucleotide;
eyposterio; virucide; protozoacide; authorotral; de.
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                             Pred. No.: 1.93e-94
Score: 825.00
Percent Similarity: 100.004
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Length: Matchem: Conservative: Mismatchem: Indelm: Gaps:

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1 Alad 6 GCTG1	66 AATT	41 Produ 126 CCGG	61 Sera 186 aggo	81 Meta 246 ATSG	101 Glua 	121 TrpP		LT 9 0994 AAN90994 mean manaoqqq.	25-MAR-2003 28-JUN-1990	Partially syn growth factor	Human acidic pAL12-haFGF;	Homo sapiene.	Key misc_feature	wise feature	mine feature		misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	muration	mutation	FT //res x //res X //res X //res Y //res Y //res Y //res X //r
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Gaps:
US-10-022-5548-4 (1-154) x AAN90994 (1-481)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-SEP-1988; 88WO-US003080.
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Sred. No.: 85.00
Sroces: Similarity: 100.004
Rest Local Sallarity: 100.004
Query March: 100.004
DB:
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Beta-endothelial cell growth factor; homeostasis; atherosclerosis; tumor; de.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene encoding human beta-undochelial call growth factor - incomposates unsell restriction stream fries at faquent intervals to facilitate cassette musquents of solected regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic gene encoding human beta-endothelial cell growth factor (BECGF).
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Matches:
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Score: No.: 825.00
Percent Statingthy: 100.00e
Bert Loral Statingthy: 100.00e
Query March: 2
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윰	257 ATGGACACCGACGGCGCTTTATACGGCTCACAGACACAAATGAGAGAAATGTTGTTCTTG 316	
ò	101 GluhrgLeuGluGluhanHisTyrhanThrTyrlleSerLysLysHallaGluLyshan 120	
셤		
à	121 TrpPheVald)yLeuLysLysAsmGlySerCysLysAsgGlyProArgThrKisTyrGly 140	
q	377 TGGTTTGTTGGCCTCAAGAAGAAGGGGGGGGGAAACGCGGTCCTCCGGACTCACTATGGC 436	
ò	141 GhLyshaileicupheicuproleuprovalsarsorasp 154	
2	437 CAGAAAGCAATCTTGTTGTCCCCCTGCCAGTCTTCTGAT 478	
RESULT ABK1059	2	
8 2	ABK10592 standard; cDNA; 630 BP.	
12.5	ABK10592;	
15	05-JUN-2002 (first entry)	
(H)	cDNA encoding human acidic FGF protein HAFGF155.	
6 B 2 3 3	8 2	
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8 8	Homo mapiens. Synthetic.	
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LL	/*tag= a /*tag= 155 protein" /product= "HaPGF 155 protein"	
ž	200214471-82.	
ž	21-FEB-2002,	
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ž	1001-004-0	
K X	15-AUG-1000; 2000US-0125466P,	
4	(PHAG-) PHAGE BIOTECHNOLOGY CORP.	
121	Stegmann IJ, Kordyum VA, Chernykh SI, Slavchenko IY, Vozianov OF;	
žž	200	
ž ž	P-PSDB; AAU76943,	
5 5	reducing a biologically active human acidic fibroblast growth factor	
: = =	nearly procedured are in promoting anguagement, involves capitalism and 25 cold transformed with a plannid having an haffor gene operably linked to a promoter.	
×		
S X	Example 1: Fig 1: 4lpp: English.	
8 8	This invention relates to a novel method for producing a biologically active human soldie fibroblast group factor (habit) moneau Fibroblast	
ខ	growth factors are potent regulators of cell proliferation,	
ខខ	differentiation and normal development and they have been shown to play a role in tumourogenesis and metastasis. Acidic fibroblast growth factor	
ខូខូ	has been shown to be potent inducers of angiogenesis. The gene for acidic fibroblast growth factor is located on human chromonome 5. The method of	
8	the invention comprises employing a plasmid having at least one copy of	
ម ម	gene, which encodes a biologically active ha?GF protein operably linked to a promoter, to transform Racherichia coli. The method is useful for	
8 8	producing recombinant or biologically active haror protein, which is	
8 8	encoding the human acidic (ibxoblast growth factor 155 process)	
ខ	C used in the method of the invention. This sequence has been chemically C synthesized using the codons which are most often used by S. coli, to	
ខ្ពស់	facilitate its expression Sequence 630 BP, 191 A, 152 C, 147 G, 140 T; O U; O Other;	
Alis	Scores:	
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Perc	milarity: 100.00% Conservative:	
See 1	100.00*	
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The invention relates to a method for enhancing the production of a consistent of the consistent activities at texts of the Enterthala follogically active protein comparing infections at texts of the Enterthala for a expressible spec with an a human middle through at least one copy of an expressible spec with an a human middle throughout protein forcer. Indeed to a phage of Polymerase processer, with a bacteriophage capable of emphasizing dailyed lysal. The school is useful for the phage dapade of superproduction of following the production of the consistent of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Naman acidic (ibrublast growth factor; phage T7 polymerase promorer;
19sts; phage dependent superproduction; synthetic; codon optimisation;
gits: de.
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ID AAK98917 standard; DNA; 630
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P-PSDB; AA019990.
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Pred. No.:
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Pscore:
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US-10-022-5548-4 (1-154) x ABK10592 (1-630)

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To secure the lumen brish even each library for close concept RCF instance as specific oligoniclectic was been designed. This oligoniclectic was based upon a factorial As expenses analyzes of the saint obscuring of ECES (see AAF7046 and AAF7041). Fig 3 to see forth for comparison the Aasequence of cyanogen broatle-ct-town downer apply and the two closes that were isolated, RCF closes RCF (AAF70534). The two closes that were isolated, RCF closes 1 and 23, were analysed in turbare detail, the worlocated sequence of these closes and the AaF7045 and AAF70451. (Updated on 35-MAX-2003 to correct PA in 18 (Let AAF70452).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete cDNA seguence of human endothelial cell growth factor (BCGF).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endothelial cell regeneration; blood vessel regeneration; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jaye M, Burgess W, Maciag T, Droban W;
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19.506

4.183

4.783

9.784

Perduce "Nera ECGF"

Produce "Acidic FOF"

7.589

7.589

7.589

7.589

7.589

7.589

7.589

7.589
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ANIOTOS:

X. ANIOTOS:

X. Caplete cDM sequence of human ender

X. Caplete cDM sequence of human ender

X. Goglete cDM sequence of human ender

X. Maniotosial cell regeneration; blood

X. Home sepient.

X. Total

Y. Total

X. Total

X. Mann endorthalist cell regeneration; blood

X. Home sepient.

Y. Total

Y. Total

X. Total

X. Mann endorthalist cell growni fercion

X. Man
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Acidic fibroblast growth factor; as. Location/Qualifiers MANSTORS Exendend, DNA; 638 BF.

AC ANASJORS Exendend, DNA; 638 BF.

AC ANASJORS

AC ANASJORS

AC ALG. (Ebroblast growth factor.

AC Ald. (Ebroblast growth factor.

AC Ald. (Ebroblast growth factor.

AC Acid. (Ebroblast growth factor.)

AC Acid Acidic fibroblast growth factor.

/*tag* a //tabel* human acidic fibroblast growth factor Fiddes JC, Abraham JA, Protter A;

Recombinant DNA encoding new fibroblast growth factor analogues - useful e.g. for accelerating wound healing and to control neowaecularisation. Disclosure, Fig 2; 44pp; English.

Sequence 638 BP; 170 A; 156 C; 168 G; 144 T; 0 U; 0 Other;

The sequence encodes human acidic fibroblast growth factor (sPGP). See also AAN93087 and AAN93089. (Updated on 25-MAR-2003 to correct PA field.)

Length: Matches: Conservative: Mismatches: Indels: Gaps: Pred. No.: 2.96=54 Score: 625.00 Percent Similarity: 100.004 Best Local Similarity: 100.004 DB: 100.004 Alignment Scores: Pred. No.:

US-10-022-554A-4 (1-154) x AAN93088 (1-638)

Borine beta-endothelial cell growth (settor (beta-2007; ANG0399) having a moil-to-0.0 to for the be purified at lease 1500 CEAL free borne brain using hepstin-Sepherose Kithingy chromotography. 2001 is useful for among other purposes, dissipancine applications and has percential in the retreatment of damaged blood vessels or other endothelial cell-liked services shown 5007 (ANT)7001 or frapement on any backmissi while oligonical cells (ANT)799 and ANT)791 to ANT)7750 whose design is based on the sequence of bovine Alpha- and bera-2009; (Updated on 22-MAN-2003 to correct Ff field.) Endothelial cell growth factor; ECOF; blood vessel; regeneration; hepatih-Schharose affinity chromatography; probe; oligomucleotide; FGP; fibroblast growth factor; ss. Implated, purified, biologically active bowine beta endothelial cell growth factor - useful to regenerate or treat damaged blood vessels. Human beta-endothelial cell growth factor. WPI; 1996-412132/41. P-PSDB; ARMO4805, ARMO4807. 19. 506
19. 506
19. 506
17. Enga b
12. 503
17. Enga b
17. Laga b
17. Laga b
17. Laga b
17. Laga c
1 (RHON) RHONE POULENC RORER PHARM INC. | Maria | Mari Disclosure: Fig 8; 28pp; English. BEUS-00835594. BTUS-00134499. 91US-00693079. Macing T, Burgess W, 03-MAR-1986; 18-DEC-1987; 29-APR-1991; 27-NOV-1991; 6 8 6 8 6 8 6 8 6 e à g à a

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XX
SQ Sequence 638 BP; 1,72 A; 165 C; 168 G; 133 T; 0 U; 0 Other;
                                                                                                                                             US-10-022-554A-4 (1-154) x AAT37503 (1-638)
         Alignment Scores: 2,96e-94
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Search completed: August 24, 2004, 23:21:50 Job time : 380 mecm

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

August 24, 2004, 23:07:08; Search time 83 Seconds (Without alignments)
1029.668 Million cell updates/sec OM protein - nucleic search, using frame_plus_p2n model

US-10-022-554A-4 825 1 ARGELITFTALTERFNLPPG......PRITHYGQKAILFLPLPVSSD 154 682709 meqs, 277475446 xemiduem Scoring rable: BLOSDM62 Xqapext 0.5 Vqapep 10.0 , Yapext 0.5 Vqapep 6.0 , Yapext 0.6 Vqapext 7.0 Dalop 6.0 , Delext 7.0 Title: Perfect score: 4 Sequence:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Ministum Match Ot Maxistum Match 100t Listing first 45 summaries

Command like parameters:

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1: /cgn2_6/ptodats/2/ins/5A_COMB.seq:*
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3: /cgn2_s/prodata/2/ins/sa_coHB.seq:*
* /cgn2_s/prodata/2/ins/sa_coHB.seq:*
5: /cgn2_s/prodata/2/ins/PCTUS_COHB.seq:*
6: /cgn2_s/prodata/2/ins/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result

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825	100.0	468	4	US-09-929-945-3	Sequence 3, Appli
825	100.0	064	•	US-09-023-655-1390	E
825	100.0	630	4	US-09-929-945-1	ų
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759.5	92.1	630	*	US-09-929-945-6	ý
759	92.0	454	ø	5175147-1	Patent No. 5175147
721	87.4	630	4	US-09-929-945-4	Sequence 4, Appli
716.5	86.8	454	٣	US-09-030-613-14	ž
716.5	86.8	454	4	US-09-451-905-14	Sequence 14, Appl
634	76.8	450	9	5437995-1	Patent No. 5437995
649.5	54.5	111	н	US-08-290-373B-16	Sequence 16, Appl
421.5	51.1	465	н	US-08-023-757-3	Sequence 3, Appli
421.5	51.1	465	ч	US-07-783-694-2	5
421.5	51,1	465	н	US-08-177-502-3	ć
115.5	50.4	465	н	US-08-023-757-1	'n
115.5	50.4	465	н	US-07-783-694-1	Ä
415.5	50.4	465	r	US-08-177-502-1	'n
113.5	50.1	174	٠	5514566-5	Patent No. 5514566
11.5	49.9	1374	•	US-09-366-009-26	Sequence 26, Appl
111.5	49.9	1374	•	US-08-809-156B-26	36,
609.5	49.6	471	н	US-08-290-373B-15	15,
901	49.3	491	н	US-07-959-369-22	55
5.5	49.0	465	n	US-08-718-904-52	25
04.5	49.0	465	*	US-09-449-249-52	g
104.5	49.0	468	S	PCT-US91-02186-1	à
104.5	49.0	477	ď	US-08-599-895-2	'n
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04.5	49.0	477	n	US-09-211-290-2	'n
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.5	0.6	411	m	US-09-322-676-2	'n
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9.5	49.0	477	7	US-09-451-905-2	ď
5.5	49.0	483	m	US-09-220-077C-1	, ,
04.5	69.0	1230	14	US-08-356-161-12	Sequence 12, Appl
04.5	49.0	1230	r	US-08-356-161-13	13,
04.5	49.0	1230	٣	US-08-718-904-53	53,
04.5	49.0	1230	•	US-09-449-249-53	Sequence 53, Appl
04.5	49.0	1230	v	PCT-US93-05702-12	
04.5	49.0	1230	'n	PCT-US93-05702-13	Sequence 13, Appl
04.5	49.0	1230	S	PCT-US95-10973A-12	12,
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			•	00-00-00-00-00-00-00-00-00-00-00-00-00-	Sequence BO, Appl

ALIGNMENTS

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Sequence 3, Application US/09929945	.on US/0992994	10	
Patent No. 6642026			
GENERAL INFORMATION:			
APPLICANT: Stegmann, Thomas	Thomas		
APPLICANT: Kordyum,	Kordyum, Vitaliy A.		
APPLICANT: Chernykh	Chernykh, Svitlana I.		
APPLICANT: Slaveher	Slavchenko, Iryna Yu.		
APPLICANT: Vozianov, Oleksandr	', Oleksandr		
TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT	SUPER PRODUCT	ION OF RECOMBINAN	F
TITLE OF INVENTION: PIBROBLAST GROWTH PACTOR	PIBROBLAST G	ROWTH PACTOR 155	
FILE REFERENCE: CVGENG, 008A	ING. 008A		
CURRENT APPLICATION NUMBER: US/09/929,945	NUMBER: US/09	/929,945	
CURRENT FILING DATE: 2001-08-15	2001-08-15		
NUMBER OF SEQ ID NOS: 8	8 ::		
SOFTWARE: FastSEQ for Windows Version 4.0	or Mindows Ver	ion 4.0	
SEQ ID NO 3			
LENGTH: 468			
TYPE: DNA			
ORGANISM: Homo mapiene	ene		
US-09-929-945-3			
Alignment Scores:			
Pred. No.:	3.858-100	Length:	468
Score:	825.00	Matches:	154
Percent Similarity:	100.004	Conservative:	0
Best Local Similarity:	100.004	Mismatches:	0
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US-10-022-554A-4 (1-154) x US-09-929-945-3 (1-468)

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TILLE OF INVERTION: FIDES, J.C.

PRILAMEN: FIDES, J.C.

PRILAMEN: FIDES, J.C.

PRILAMEN: PRICES, J.C.

TILLE OF INVERTION: REAME MALIC GROWTH

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STATE: OA STATE: Iength: Matchem: Conservative: Mismatchem: Indelm: Gapm: US-10-022-554A-4 (1-154) x US-09-098-628-3 (1-638) Alignment Scores: 6.16-100 Score: 6.5.00 Percent Stallardy: 100.004 Best Incal Stallardy: 100.004 Query March: 1 õ a à g à å ò đ â 3 4 5 6 5 à

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Score: 2.86e-98
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Score: No.: 759.50
Fercent Smillarity: 94.131
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Query March: 4
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Pred. No.: 759.00
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US-10-022-554A-4 (1-154) x US-09-451-905-14 (1-454)

Iength: Marches: Conservative: Mismatches: Indels: Gaps:

Pred. No.: 8.62s-86 Score: 716.50 Percenc Similarity: 91.04* Best Local Similarity: 92.41* Oper Match: 4.85*

Alignment Scores: Pred. No.:

FILE REFERENCE 20013, 402,95
CURSENT FILED ANTE: 1879,145,95
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HOWER OF SEQ ID MOS: 48-11-0;
SEQ ID MOS 14-120 for Kindows Version 4.0
SEQ ID NO 18-120 for Kindows Version 4.0
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sequence of Apparation of Occasions of Section 1990 of September 1	Patent No. 5310883 GRANAL IMPORATION REPLICANT Andrew P. Seddon, Peter Bollen and
APPLICANT: Bohlen Dr., Peter APPLICANT: Glaman Dr., Nakon TITL OF NYENTION: Chimacze Fibroblast Growth Pactors	; APELCANT: Vakov dlurman; ; TITEZ OF INVENTION: Chimeric Fibroblas: Growth ; TITEZ OF INVENTION: Chimeric Fibroblas: Growth ; TITEZ OF INVENTION: Rescore
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APPLICATION NUMBER: US/08/023,757 FILIND DATE: 36-PEB-1993	SOFTWARE: 4 CURRENT APPLICATION DATA:
CLASSIFICATION: 530 PRIOR APPLICATION DATA:	APPLICATION WIMBER: US/07/781,694 ; FILING DATE: 19911104
APPLICATION NIMBER: US/07/615-202 FILING DATE: 23-MOV-1990 APPOREN/JARRY INFORMATION:	: CLASSICATION: 435 : PRICA APPLICATION DATA: : APPLICATION UNDER:
ALONENTARIA INTORNALION: NAME: Thevode Dr., Sweelle J. REGISTRATION NUMBER: 31,145	FILING DATE: ATTORNEY AGENT INFORMATION:
REFERENCE/INOCKET NUMBER: 11,219-00 TELECOMONICATION INPOSETION:	NAME: Taewdow, Katelle J., Dr. ; REGISTRATION WUMBER: 31,145 ; REFERENCE/POCKET WITHERR: 31,215-01
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

Search completed: August 25, 2004, 01:15:15 Job time : 420 mes

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	(HUMAN);, mRNA mequence.
ACCESSION	A1590078
VERSION	AIS90078.1 GI:4599126
KEYWORDS	. 158
SOURCE	Homo sapiena (human)
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	Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Ruteleostomi.
	Mannalia, Sutheria, Primates: Catarrhin: Hominidae, Romo
REFERENCE	1 (bases 1 to 534)
AUTHORS	NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgan
TITLE	National Cancer Institute / National Institute of Neurological
	Disorders and Stroke, Brain Tumor Genome Anatomy Project
	(CGAP/BIGAP), Tumor Gene Index
JOURNAL	Unpublished (1998)
COMMENT	Contact: Robert Strausberg, Ph.D.
	Smail: cgapbs-r@mail.nih.gov
	Timene Procurement: David N. Louis, M.D., Myrns R. Rosenfeld M.D.
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Conservative:
Mismatches:
Indels:
Gaps: US-10-022-554A-4 (1-154) x AIS98078 (1-534) Pred. No.: 9.11e-96 Score: 825.00 Percent Similarity: 100.004 Best Local Similarity: 100.004 Obery Match: 9 Alignment Scores: Pred. No.: RESULT 2 BISS8390 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM AUTHORS TITLE JOURNAL COMMENT DRIGIN ä g ď ò 3 A 3 A à à g 8 8 g

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Pred. No.:	Pred. No.:	2.23e-95	Length:	1014
Score:		825.00	Matches:	154
Percent	Percent Similarity:		Conservative:	0
Best Local S	Best Local Similarity:	100.004	Missatches	
DB:		12	Gaps:	
US-10-0	US-10-022-554A-4 (1-154) x BM809005 (1-1014)	4) × BM809005	(1-1014)	
ò	1 AlaGluGl	yGluIleThri	heThralaLeuThrGlu	AlacludyGlulleThrThrPheThrAlaLeuThrGluLymPheAmheuProProGly 20
£.	186 GCTGAAGG	GGAAATCACCACCA	TCACAGCCCTGACCGAG	GCTGAAGGGAAATCACCACCATCACCCTGACGGAGAATTAATCTGCCTCCAGGG 245
'n	21 AsnTyrLy	"LysProLysLeuI	euTyrCysSerMenGly	AsnTyrLysLysLysLeuLeuTyrCysSerAsnGlyGlyHisPheLeuAgileLeu 40
a	246 AATTACAA	GAAGCCCAAACTCC	TCTACTGTAGCAACGGG	AATTACAAGAAGCCAAACTCCTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTT 305
š	41 Produpel	yThrValAmpGlyJ	hrargaspargserasp	ProkapülyThrValkapülyThrkrgkapkrgSerkapülnHisileGlnheuülnLeu 60
d d	306 CCGGATGG	CACAGTGGATGGG	CARGGGACAGGAGCGAC	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
ä	61 Seralagi	uSerValGlyGluV	alTyrileLysSerThr	SerklaGluSerValOlyGluValTyrIleLysSerThrGluThrGlyGlnTyrLeukla 80
QQ.	366 AGTGCGGA	AAGCGTGGGGGAGG	TGTATATAAGAGTACO	
λio	81 MechapTh	rAspGlyLeuLeuT	yrGlySerGlhThrPro	MeckapThrAspGlyLeuLeuTyrGlySerGlbThrProAsnGluGluGysLeuPheLeu 100
eg.	425 ATGGACAC	CGACGGGCTTTTAT	ACGGCTCACAGACACCA	ATGGACCCACGGCTTTTATACGGCTCACAGACGAAATGAGGAATGTTTGTT
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TITLE	Zhu, Q., Person, C. and Sands, A.T. Whil kinsse deficiency lowers blood pressure in mice: a gene-trap
7	Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
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Carninci,P. and Mayashizaki,Y.
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Nature 409, 665-690 (2001)

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